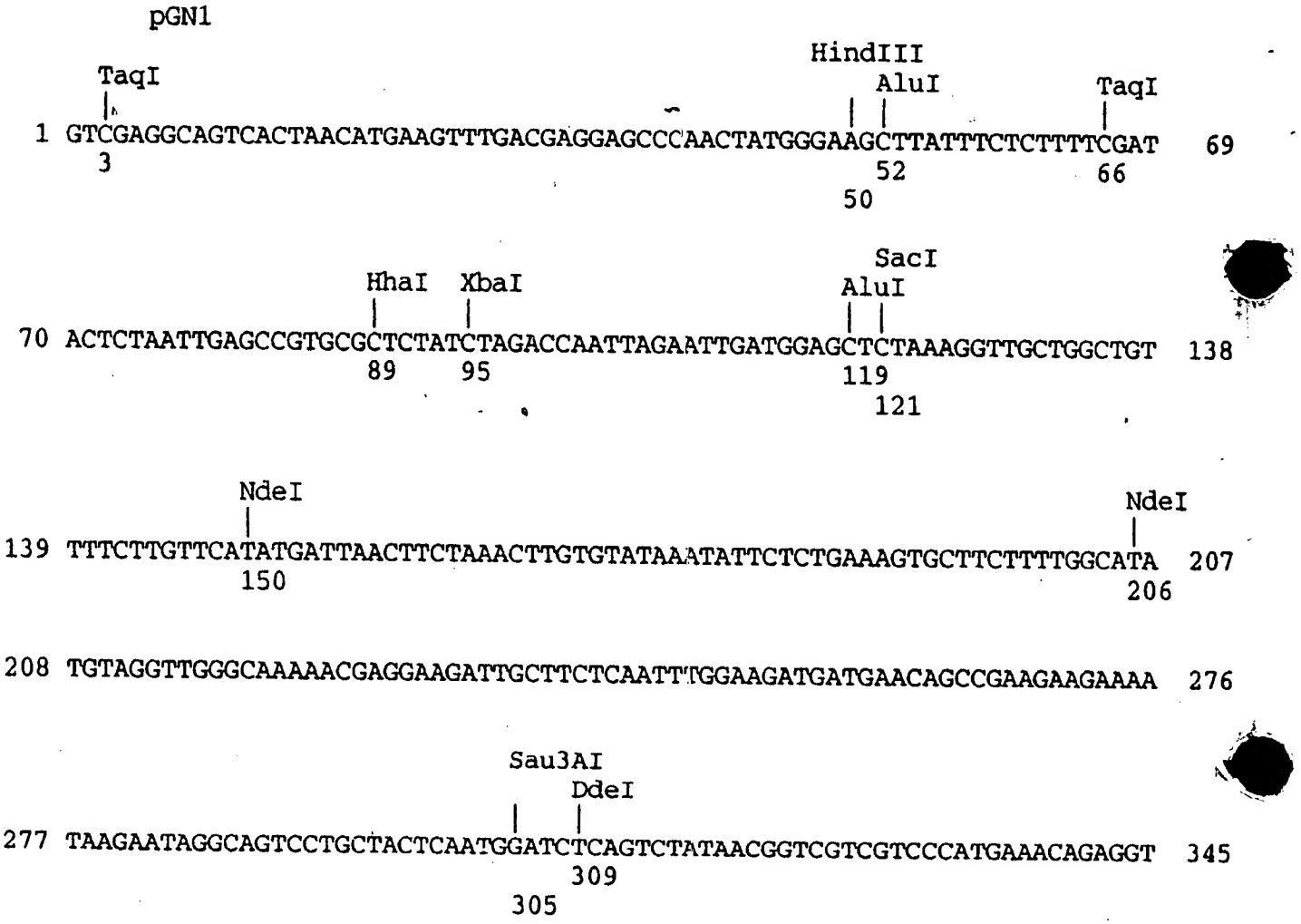

pGN1
TaqI
HindIII
AluI
TaqI
1 GTCGAGGCAGTCACTAACATGAAGTTTGACGAGGAGCCCAACTATGGGAAGCTTATTTCTCTTTTCGAT 69
3
52
66
50
SacI
HhaI
XbaI
AluI
70 ACTCTAATTGAGCCGTGCGCTCTATCTAGACCAATTAGAATTGATGGAGCTCTAAAGGTTGCTGGCTGT 138
89
95
119
121
NdeI
NdeI
139 TTTCTTGTTCATATGATTAACTTCTAAACTTGTGTATAAATATTCTCTGAAAGTGCTTCTTTTGGCATA 207
150
206
208 TGTAGGTTGGGCAAAAACGAGGAAGATTGCTTCTCAATTTGGAAGATGATGAACAGCCGAAGAAGAAAA 276
Sau3AI
DdeI
277 TAAGAATAGGCAGTCCTGCTACTCAATGGATCTCAGTCTATAACGGTCGTCGTCCCATGAAACAGAGGT 345
309
305

FIG. 1A

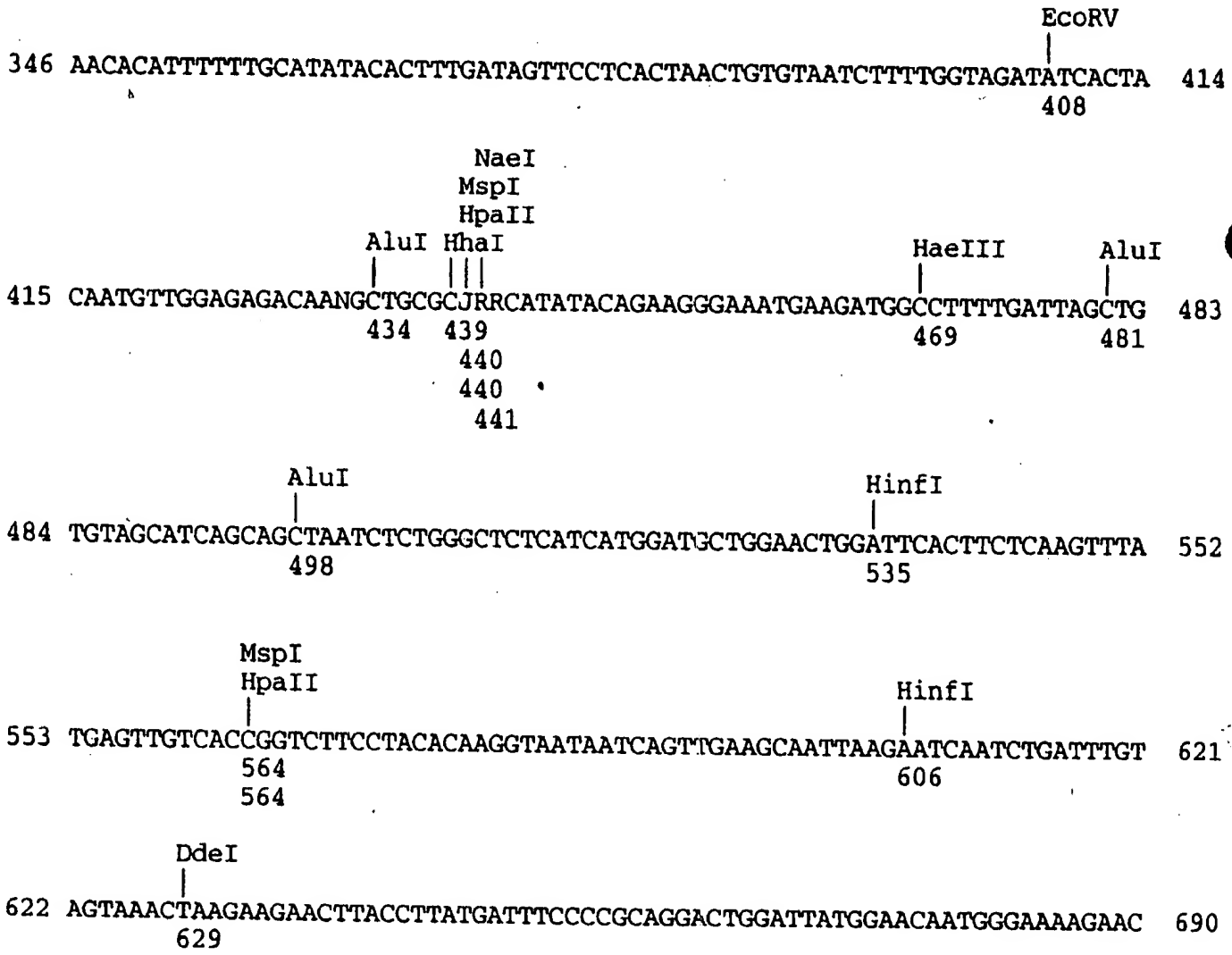

EcoRV
346 AACACATTTTTTGCATATACACTTTGATAGTTCCTCACTAACTGTGTAATCTTTTGGTAGATATCACTA 414
408
NaeI
MspI
HpaII
AluI HhaI
HaeIII AluI
415 CAATGTTGGAGAGACAANGCTGCGCJRRCATATACAGAAGGGAAATGAAGATGGCCTTTTGATTAGCTG 483
434 439
469 481
440
440
441
AluI
HinfI
484 TGTAGCATCAGCAGCTAATCTCTGGGCTCTCATCATGGATGCTGGAACTGGATTCACTTCTCAAGTTTA 552
498
535
MspI
HpaII
HinfI
553 TGAGTTGTCACCGGTCTTCCTACACAAGGTAATAATCAGTTGAAGCAATTAAGAATCAATCTGATTTGT 621
564
564
606
DdeI
622 AGTAAACTAAGAAGAACTTACCTTATGATTTCCCCGCAGGACTGGATTATGGAACAATGGGAAAAGAAC 690
629

FIG. 1B

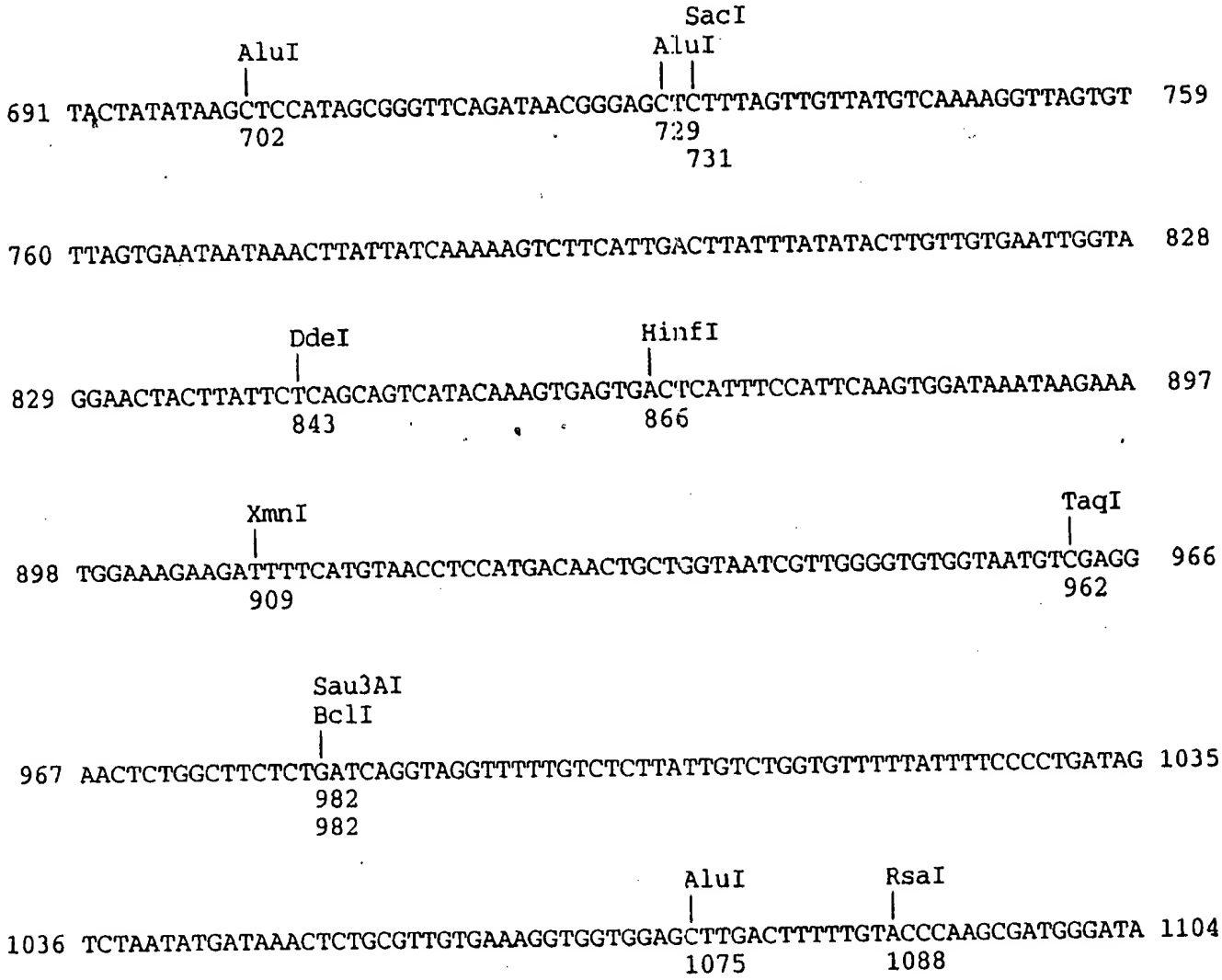

SacI
AluI
AluI
691 TACTATATAAGCTCCATAGCGGGTTCAGATAACGGGAGCTCTTTAGTTGTTATGTCAAAAGGTTAGTGT 759
702
729
731
760 TTAGTGAATAATAAACTTATTATCAAAAAGTCTTCATTGACTTATTTATATACTTGTTGTGAATTGGTA 828
DdeI
HinfI
829 GGAACTACTTATTCTCAGCAGTCATACAAAGTGAGTGACTCATTTCCATTCAAGTGGATAAATAAGAAA 897
843
866
XmnI
TaqI
898 TGGAAAGAAGATTTTCATGTAACCTCCATGACAACTGCTGGTAATCGTTGGGGTGTGGTAATGTCGAGG 966
909
962
Sau3AI
BclI
967 AACTCTGGCTTCTCTGATCAGGTAGGTTTTTGTCTCTTATTGTCTGGTGTTTTTATTTTCCCCTGATAG 1035
982
982
AluI
RsaI
1036 TCTAATATGATAAACTCTGCGTTGTGAAAGGTGGTGGAGCTTGACTTTTTGTACCCAAGCGATGGGATA 1104
1075
1088

FIG. 1C

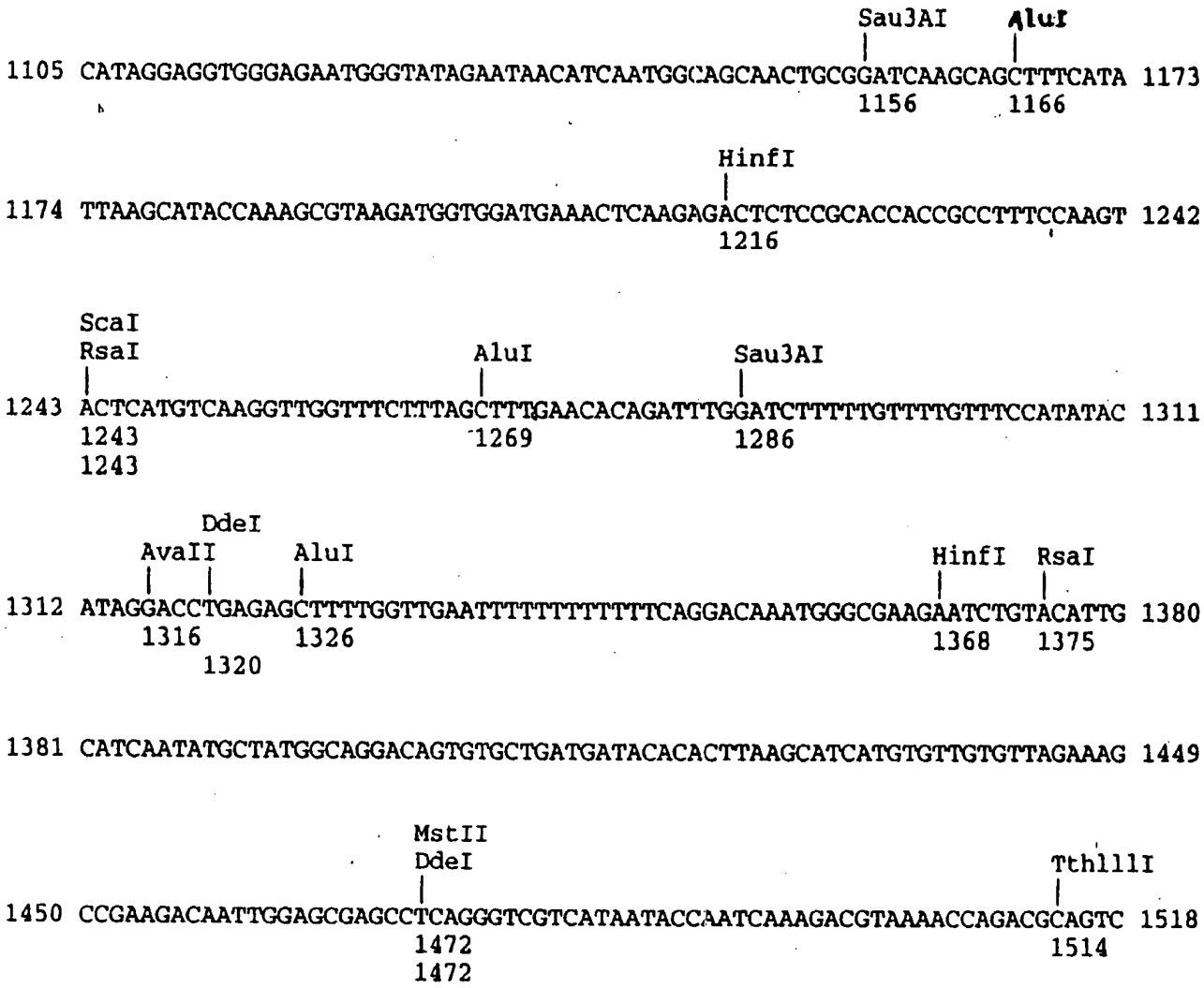

Sau3AI
AluI
1105 CATAGGAGGTGGGAGAATGGGTATAGAATAACATCAATGGCAGCAACTGCGGATCAAGCAGCTTTCATA 1173
1156
1166
HinfI
1174 TTAAGCATACCAAAGCGTAAGATGGTGGATGAAACTCAAGAGACTCTCCGCACCACCGCCTTTCCAAGT 1242
1216
ScaI
RsaI
AluI
Sau3AI
1243 ACTCATGTCAAGGTTGGTTTCTTTAGCTTTGAACACAGATTTGGATCTTTTTGTTTTGTTTCCATATAC 1311
1243
1269
1286
1243
DdeI
AvaII
AluI
HinfI
RsaI
1312 ATAGGACCTGAGAGCTTTTGGTTGAATTTTTTTTTTTTCAGGACAAATGGGCGAAGAATCTGTACATTG 1380
1316
1326
1368
1375
1320
1381 CATCAATATGCTATGGCAGGACAGTGTGCTGATGATACACACTTAAGCATCATGTGTTGTGTTAGAAAG 1449
MstII
DdeI
TthlllI
1450 CCGAAGACAATTGGAGCGAGCCTCAGGGTCGTCATAATACCAATCAAAGACGTAAAACCAGACGCAGTC 1518
1472
1514
1472

FIG. 1D

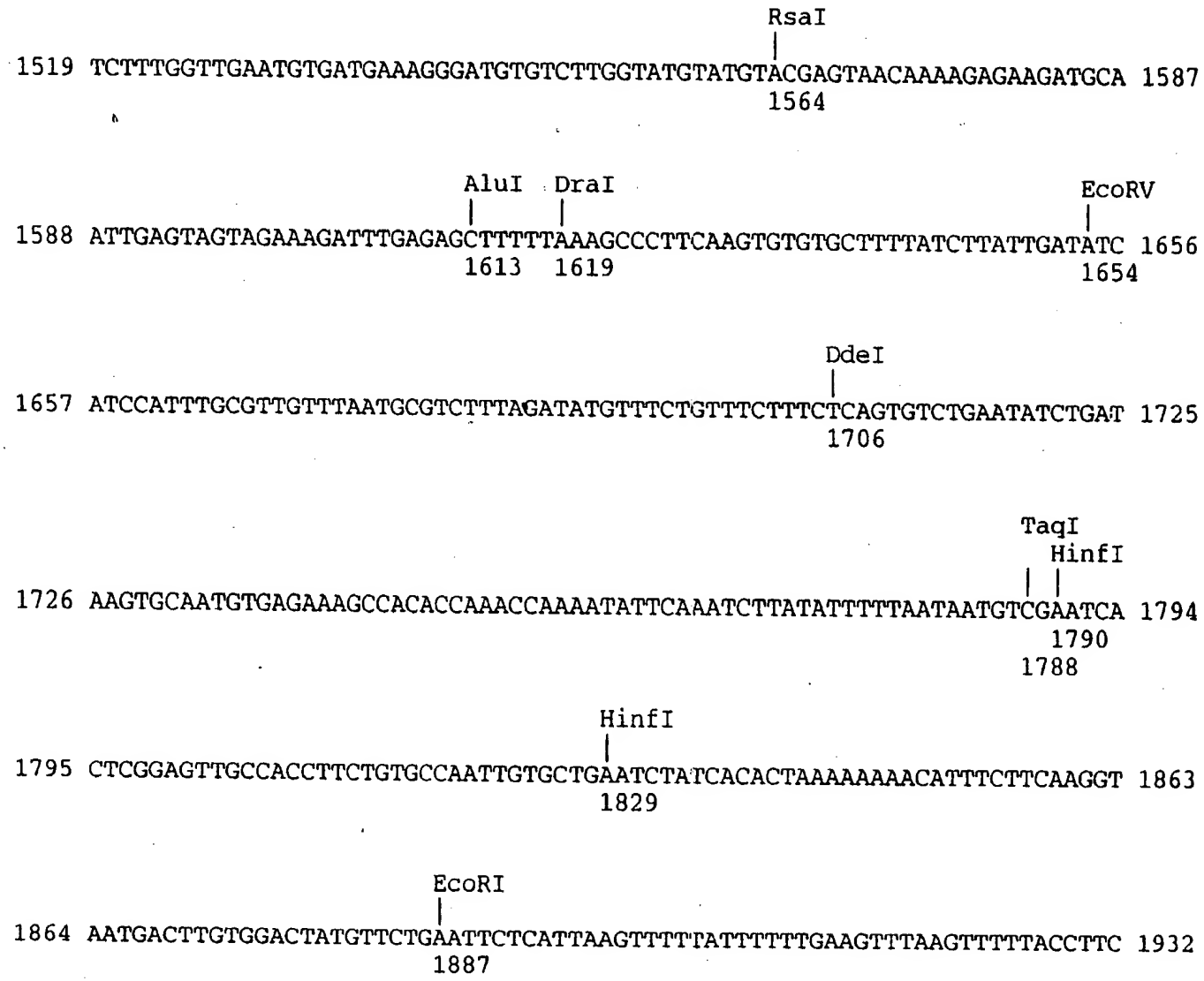


FIG. 1E

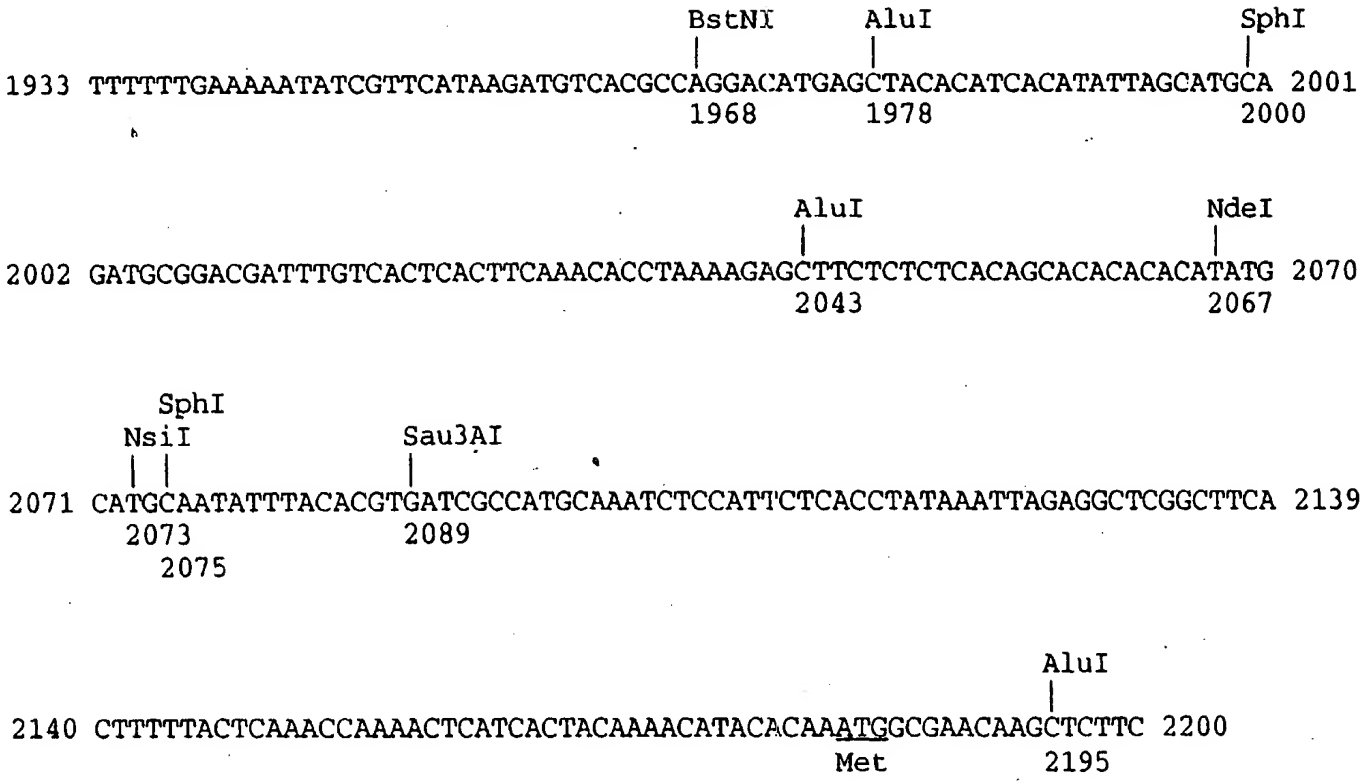


FIG. 1F

Lambda CGN1-2

NCG-186 Linear   LENGTH = 4325

```
   XhoI                                                     HindIII
    TaqI                                                     AluI        TaqI
   AvaI                                                     |  |          |
   ||
1  CTCGAGGCAGTCACTAACATGAAGTTTGACGAGGAGCCCAACTATGGGAAGCTTATTTCTCTTTTCGAT   69

   2                                                          52          66
    3                                                       50
   2

                       HhaI   XbaI                          SacI
                        |      |                           AluI
                                                           |  |
70  ACTCTAATTGAGCCGTGCGCTCTATCTAGACCAATTAGAATTGATGGAGCTCTAAAGGTTGCTGGCTGT   138

                       89     95                           119
                                                            121

              NdeI                                                    NdeI
               |                                                       |
139 TTTCTTGTTCATATGATTAACTTCTAAACTTGTGTATAAATATTCTCTGAAAGTGCTTCTTTTGGCATA   207

              150                                                     206

208 TGTAGGTTGGGCAAAAACGAGGAAGATTGCTTCTCAATTTGGAAGAGGATGAACAGCCGAAGAAGAAAA   276

                             Sau3AI
                               DdeI
                             |  |
277 TAAGAATAGGCAGTCCTGCTACTCAATGGATCTCAGTCTATAACGGTCGTCGTCCCATGAAACAGAGGT   345

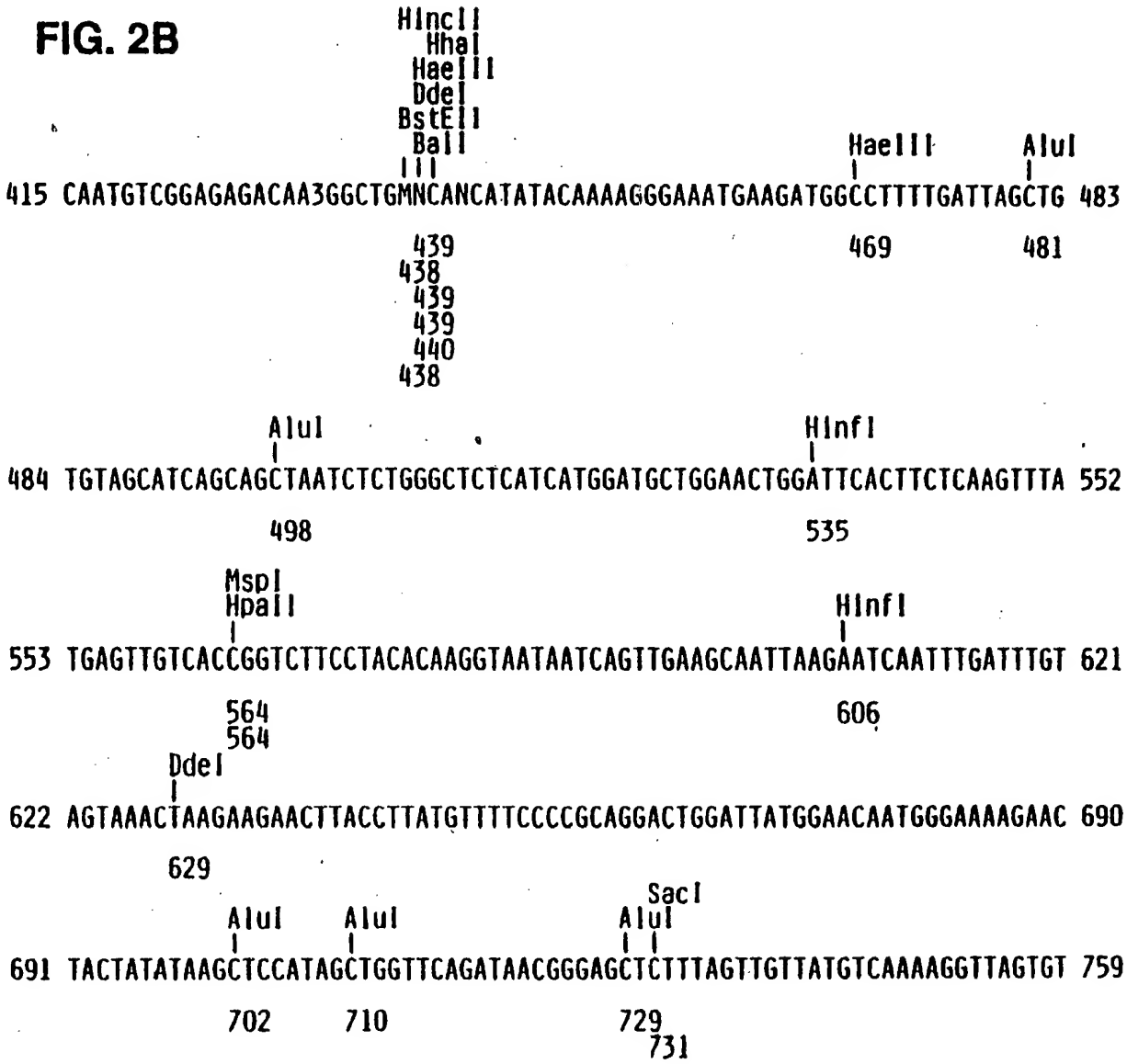
                               309
                             305

                                                                   EcoRV
                                                                    |
346 AAAACATTTTTTGCATATACACTTTGAAAGTTCCTCACTAACTGTGTAATCTTTTGGTAGATATCACTA   414

                                                                   408
```

FIG. 2A

FIG. 2B



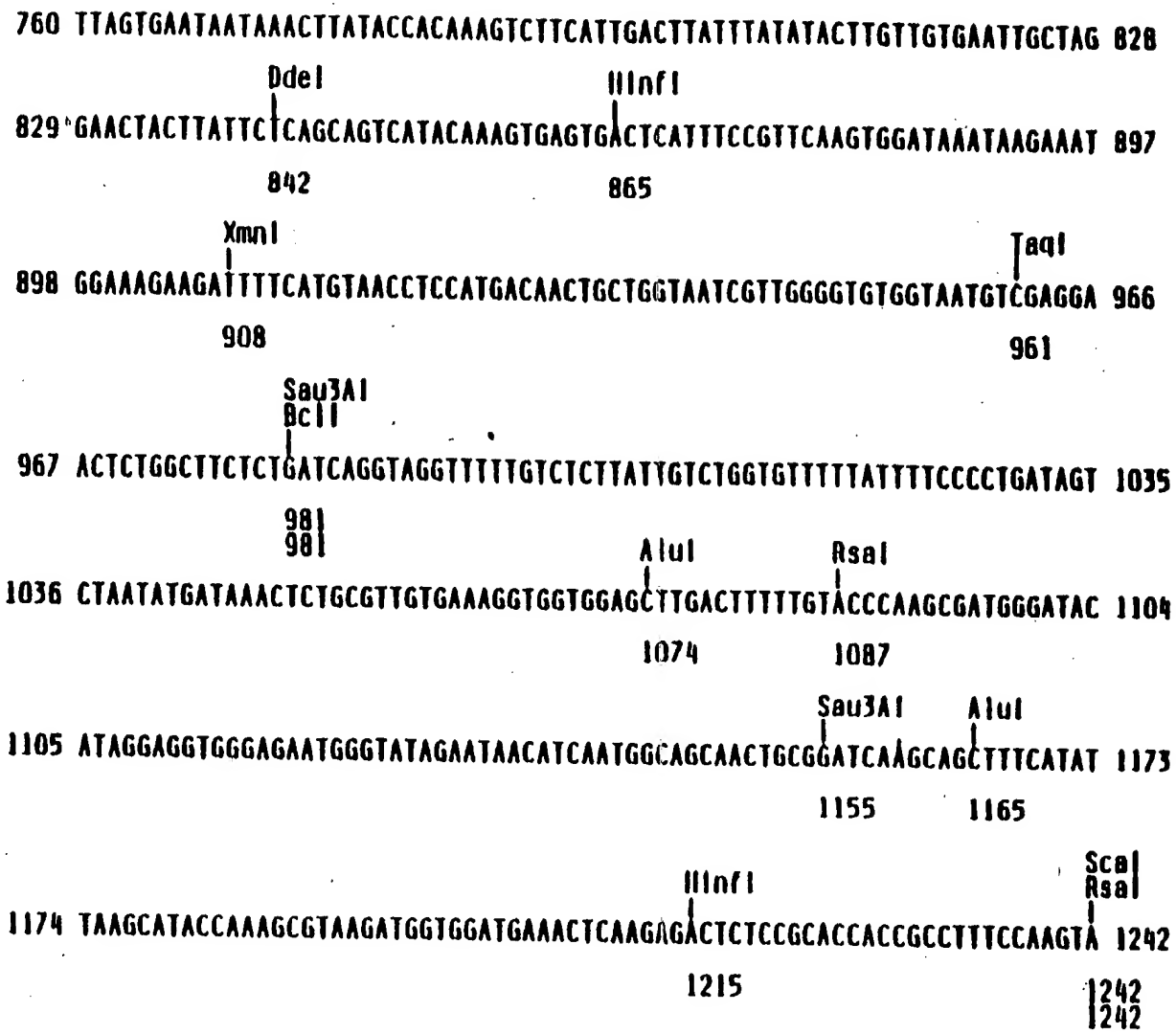

760 TTAGTGAATAATAAACTTATACCACAAAGTCTTCATTGACTTATTTATATACTTGTTGTGAATTGCTAG 828
DdeI
HinfI
829 GAACTACTTATTCTCAGCAGTCATACAAAGTGAGTGACTCATTTCCGTTCAAGTGGATAAATAAGAAAT 897
842
865
XmnI
TaqI
898 GGAAAGAAGATTTTCATGTAACCTCCATGACAACTGCTGGTAATCGTTGGGGTGTGGTAATGTCGAGGA 966
908
961
Sau3AI
BclI
967 ACTCTGGCTTCTCTGATCAGGTAGGTTTTTGTCTCTTATTGTCTGGTGTTTTTATTTTCCCCTGATAGT 1035
981
981
AluI
RsaI
1036 CTAATATGATAAACTCTGCGTTGTGAAAGGTGGTGGAGCTTGACTTTTTGTACCCAAGCGATGGGATAC 1104
1074
1087
Sau3AI
AluI
1105 ATAGGAGGTGGGAGAATGGGTATAGAATAACATCAATGGCAGCAACTGCGGATCAAGCAGCTTTCATAT 1173
1155
1165
HinfI
ScaI
RsaI
1174 TAAGCATACCAAAGCGTAAGATGGTGGATGAAACTCAAGAGACTCTCCGCACCACCGCCTTTCCAAGTA 1242
1215
1242
1242

FIG. 2C

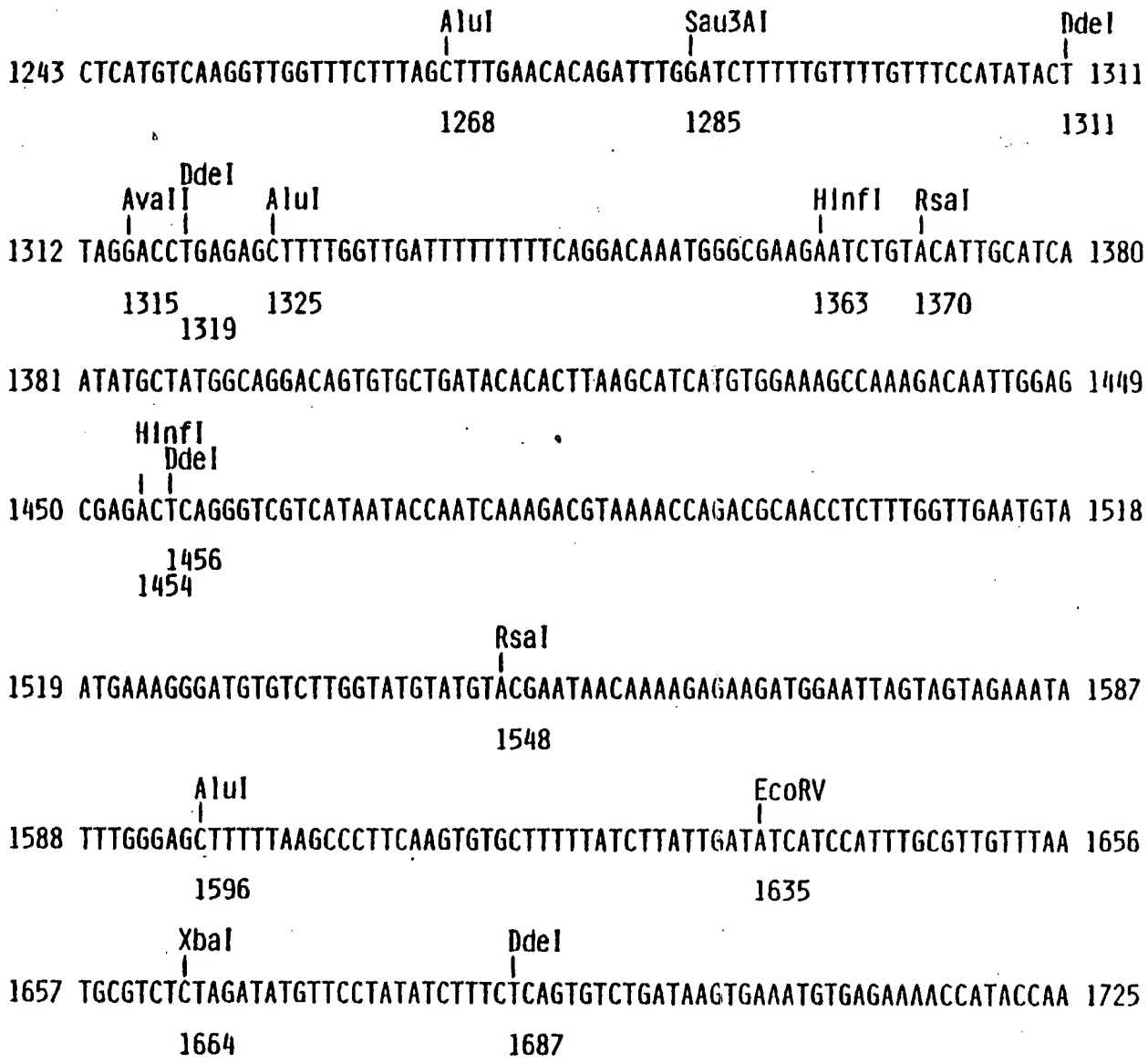

AluI
Sau3AI
DdeI
1243 CTCATGTCAAGGTTGGTTTCTTTAGCTTTGAACACAGATTTGGATCTTTTTGTTTTGTTTCCATATACT 1311
1268
1285
1311
DdeI
AvaII
AluI
HinfI
RsaI
1312 TAGGACCTGAGAGCTTTTGGTTGATTTTTTTTTCAGGACAAATGGGCGAAGAATCTGTACATTGCATCA 1380
1315
1319
1325
1363
1370
1381 ATATGCTATGGCAGGACAGTGTGCTGATACACACTTAAGCATCATGTGGAAAGCCAAAGACAATTGGAG 1449
HinfI
DdeI
1450 CGAGACTCAGGGTCGTCATAATACCAATCAAAGACGTAAAACCAGACGCAACCTCTTTGGTTGAATGTA 1518
1456
1454
RsaI
1519 ATGAAAGGGATGTGTCTTGGTATGTATGTACGAATAACAAAAGAGAAGATGGAATTAGTAGTAGAAATA 1587
1548
AluI
EcoRV
1588 TTTGGGAGCTTTTTAAGCCCTTCAAGTGTGCTTTTTATCTTATTGATATCATCCATTTGCGTTGTTTAA 1656
1596
1635
XbaI
DdeI
1657 TGCGTCTCTAGATATGTTCCTATATCTTTCTCAGTGTCTGATAAGTGAAATGTGAGAAAACCATACCAA 1725
1664
1687

FIG. 2D


HInfI
1726 ACCAAAATATTCAAATCTTATTTTTAATAATGTTGAATCACTCGGAGTTGCCACCTTCTGTGCCAATTG 1794
1761
HInfI
EcoRI
1795 TGCTGAATCTATCACACTAGAAAAAAACATTTCTTCAAGGTAATGACTTGTGGACTATGTTCTGAATTC 1863
1800
1859
1864 TCATTAAGTTTTTATTTTCTGAAGTTTAAGTTTTTACCTTCTGTTTTGAAATATATCGTTCATAAGATG 1932
SphI
BstNI
AluI
Sau3AI
1933 TCACGCCAGGACATGAGCTACACATCGCACATAGCATGCAGATCAGGACGATTTGTCACTCACTTCAAA 2001
1940
1950
1973
1971
SphI
DdeI
AluI
HhaI
NdeI
NsiI
Sau3AI
2002 CACCTAAGAGCTTCTCTCTCACAGCGCACACACATATGCATGCAATATTTACACGTGATCGCCATGCAA 2070
2006
2012
2028
2036
2042
2044
2058
2071 ATCTCCATTCTCACCTATAAATTAGAGCCTCGGCTTCACTCTTTACTCAAACCAAAACTCATCACTACA 2139
AluI
2140 GAACATACACAAATGGCGAACAAGCTCTTCCTCGTCTCGGCAACTCTCGCCTTGTTCTTCCTTCTCACC 2208
METAlaAsnLysLeuPheLeuValSerAlaThrLeuAlaLeuPhePheLeuLeuThr
2164

FIG. 2E

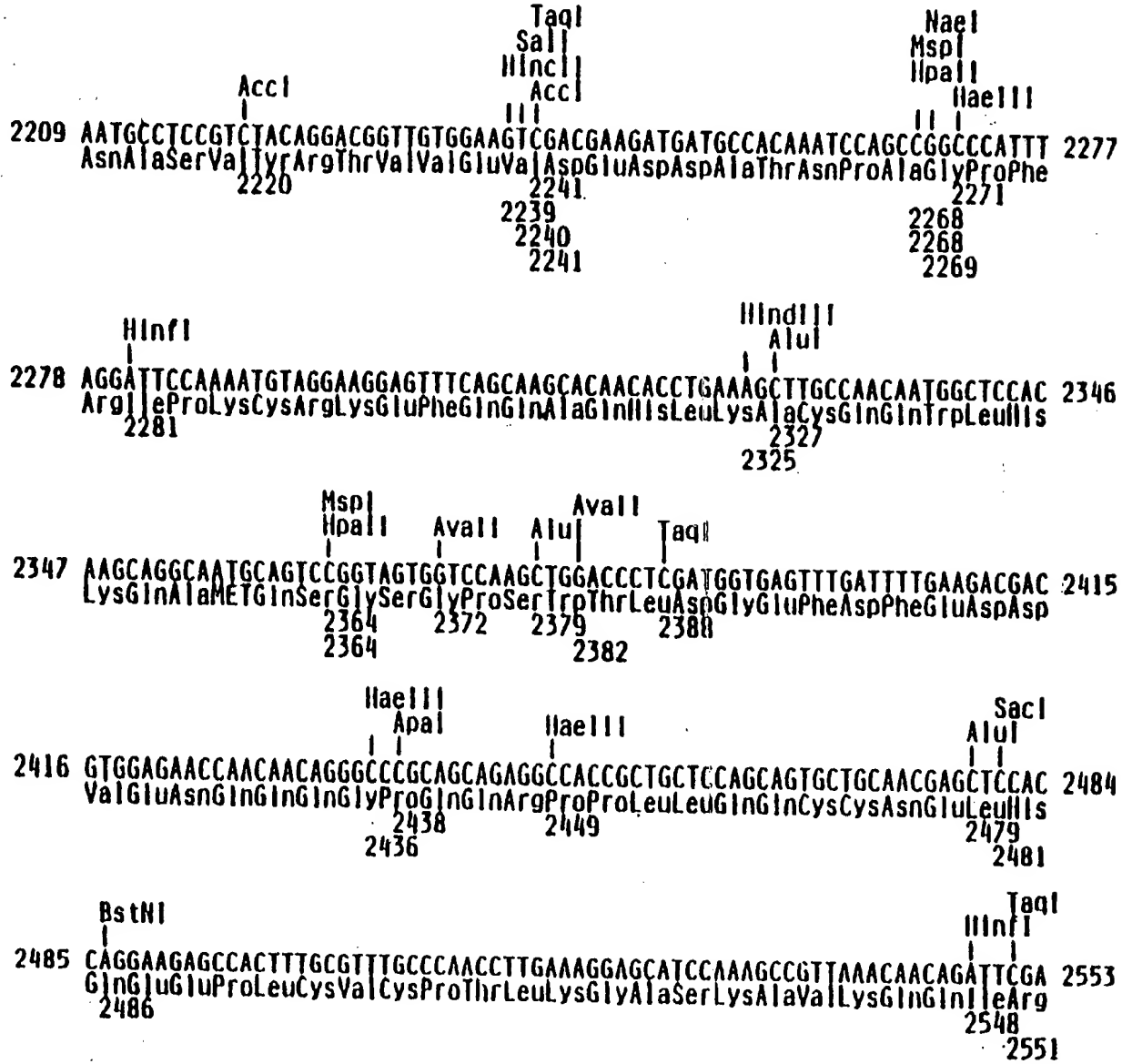

TaqI
SalI
HincII
AccI
AccI
NaeI
MspI
HpaII
HaeIII
2209 AATGCCTCCGTCTACAGGACGGTTGTGGAAGTCGACGAAGATGATGCCACAAATCCAGCCGGCCCATTT 2277
AsnAlaSerValTyrArgThrValValGluValAspGluAspAspAlaThrAsnProAlaGlyProPhe
2220
2241
2239
2240
2241
2271
2268
2268
2269
HinfI
HindIII
AluI
2278 AGGATTCCAAAATGTAGGAAGGAGTTTCAGCAAGCACAACACCTGAAAGCTTGCCAACAATGGCTCCAC 2346
ArgIleProLysCysArgLysGluPheGlnGlnAlaGlnHisLeuLysAlaCysGlnGlnTrpLeuHis
2281
2327
2325
MspI
HpaII
AvaII
AvaII
AluI
TaqI
2347 AAGCAGGCAATGCAGTCCGGTAGTGGTCCAAGCTGGACCCTCGATGGTGAGTTTGATTTTGAAGACGAC 2415
LysGlnAlaMETGlnSerGlySerGlyProSerTrpThrLeuAspGlyGluPheAspPheGluAspAsp
2364
2364
2372
2379
2382
2388
HaeIII
ApaI
HaeIII
SacI
AluI
2416 GTGGAGAACCAACAACAGGGCCCGCAGCAGAGGCCACCGCTGCTCCAGCAGTGCTGCAACGAGCTCCAC 2484
ValGluAsnGlnGlnGlnGlyProGlnGlnArgProProLeuLeuGlnGlnCysCysAsnGluLeuHis
2438
2436
2449
2479
2481
BstNI
TaqI
HinfI
2485 CAGGAAGAGCCACTTTGCGTTTGCCCAACCTTGAAAGGAGCATCCAAAGCCGTTAAACAACAGATTCGA 2553
GlnGluGluProLeuCysValCysProThrLeuLysGlyAlaSerLysAlaValLysGlnGlnIleArg
2486
2548
2551

FIG. 2F

```
2554 CAACAACAGGGACAACAAATGCAGGGACAGCAGATGCAGCAAGTGATTAGCCGTATCTACCAGACCGCT 2622
     GlnGlnGlnGlyGlnGlnMETGlnGlyGlnGlnMETGlnGlnValIleSerArgIleTyrGlnThrAla

                    AluI                                                  BstNI
                    |                                                     |
2623 ACGCACTTACCTAGAGCTTGCAACATCAGGCAAGTTAGCATTTGCCCCTTCCAGAAGACCATGCCTGGG 2691
     ThrHisLeuProArgAlaCysAsnIleArgGlnValSerIleCysProPheGlnLysThrMETProGly
                    2639                                                  2688

       MspI
       HpaII
     HaeIII
       ApaI           HinfI                XhoI
                                             TaqI
                                           AvaI        AccI
     | |              |                    ||          |
2692 CCCGGCTTCTACTAGATTCCAAACGAATATCCTCGAGAGTGTGTATACCACGGTGATATGAGTGTGGTT 2760
     ProGlyPheTyr
       2694           2707                 2724        2736
     2692                                    2725
       2694                                2724
       2694

                 HincII                                       RsaI
                 |                                            |
2761 GTTGATGTATGTTAACACTACATAGTCATGGTGTGTGTTCCATAAATAATGTACTAATGTAATAAGAAC 2829
                 2771                                         2813

             AccI
             |
2830 TACTCCGTAGACGGTAATAAAAGAGAAGTTTTTTTTTTTACTCTTGCTACTTTCCTATAAAGTGATGAT 2898
             2838

                                                                ScaI
                                                                RsaI
                                                                |
2899 TAACAACAGATACACCAAAAAGAAAACAATTAATCTATATTCACAATGAAGCAGTACTAGTCTATTGAA 2967
                                                                2954
                                                                2954
```

FIG. 2G

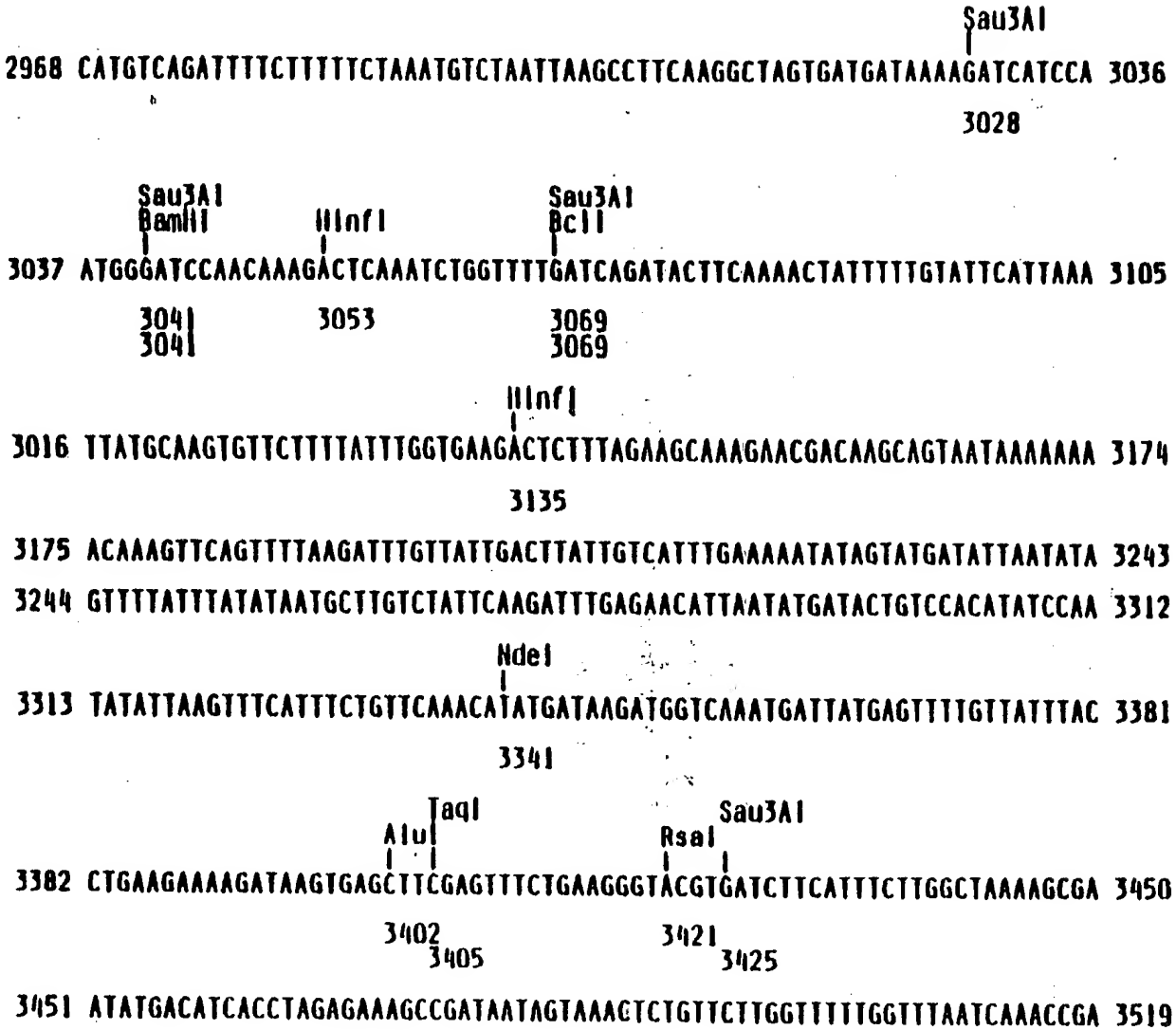

Sau3AI
2968 CATGTCAGATTTTCTTTTTCTAAATGTCTAATTAAGCCTTCAAGGCTAGTGATGATAAAAGATCATCCA 3036
3028
Sau3AI
BamHI
HInfI
Sau3AI
BclI
3037 ATGGGATCCAACAAAGACTCAAATCTGGTTTTGATCAGATACTTCAAAACTATTTTTGTATTCATTAAA 3105
3041
3041
3053
3069
3069
HInfI
3016 TTATGCAAGTGTTCTTTTATTTGGTGAAGACTCTTTAGAAGCAAAGAACGACAAGCAGTAATAAAAAAA 3174
3135
3175 ACAAAGTTCAGTTTTAAGATTTGTTATTGACTTATTGTCATTTGAAAAATATAGTATGATATTAATATA 3243
3244 GTTTTATTTATATAATGCTTGTCTATTCAAGATTTGAGAACATTAATATGATACTGTCCACATATCCAA 3312
NdeI
3313 TATATTAAGTTTCATTTCTGTTCAAACATATGATAAGATGGTCAAATGATTATGAGTTTTGTTATTTAC 3381
3341
TaqI
Sau3AI
AluI
RsaI
3382 CTGAAGAAAAGATAAGTGAGCTTCGAGTTTCTGAAGGGTACGTGATCTTCATTTCTTGGCTAAAAGCGA 3450
3402
3405
3421
3425
3451 ATATGACATCACCTAGAGAAAGCCGATAATAGTAAAGTCTGTTCTTGGTTTTTGGTTTAATCAAACCGA 3519

FIG. 2H

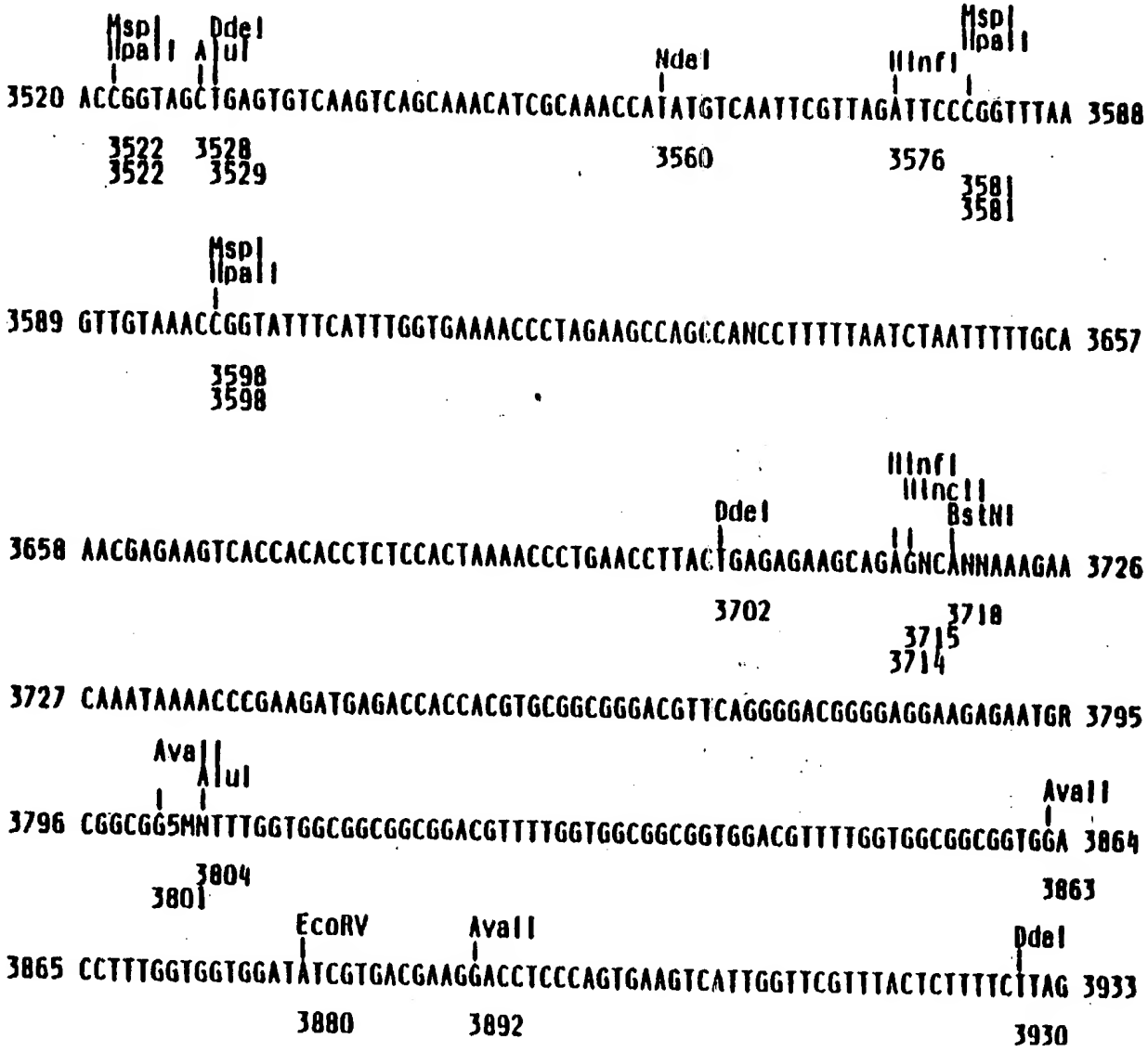

MspI
pa1 I
A
DdeI
ul
NdeI
IIInfI
MspI
pa1 I
3520 ACCGGTAGCTGAGTGTCAAGTCAGCAAACATCGCAAACCATATGTCAATTCGTTAGATTCCCGGTTTAA 3588
3522
3528
3522
3529
3560
3576
358
358
MspI
pa1 I
3589 GTTGTAAACCGGTATTTCATTTGGTGAAAACCCTAGAAGCCAGCCANCCTTTTTAATCTAATTTTTGCA 3657
3598
3598
IIInfI
IIInc II
DdeI
BstNI
3658 AACGAGAAGTCACCACACCTCTCCACTAAAACCCTGAACCTTACTGAGAGAAGCAGAGNCANNAAAGAA 3726
3702
3718
3715
3714
3727 CAAATAAAACCCGAAGATGAGACCACCACGTGCGGCGGGACGTTCAGGGGACGGGGAGGAAGAGAATGR 3795
AvaII
A ul
AvaII
3796 CGGCGG5MNTTTGGTGGCGGCGGCGGACGTTTTGGTGGCGGCGGTGGACGTTTTGGTGGCGGCGGTGGA 3864
3804
3801
3863
EcoRV
AvaII
DdeI
3865 CCTTTGGTGGTGGATATCGTGACGAAGGACCTCCCAGTGAAGTCATTGGTTCGTTTACTCTTTTCTTAG 3933
3880
3892
3930

FIG. 21

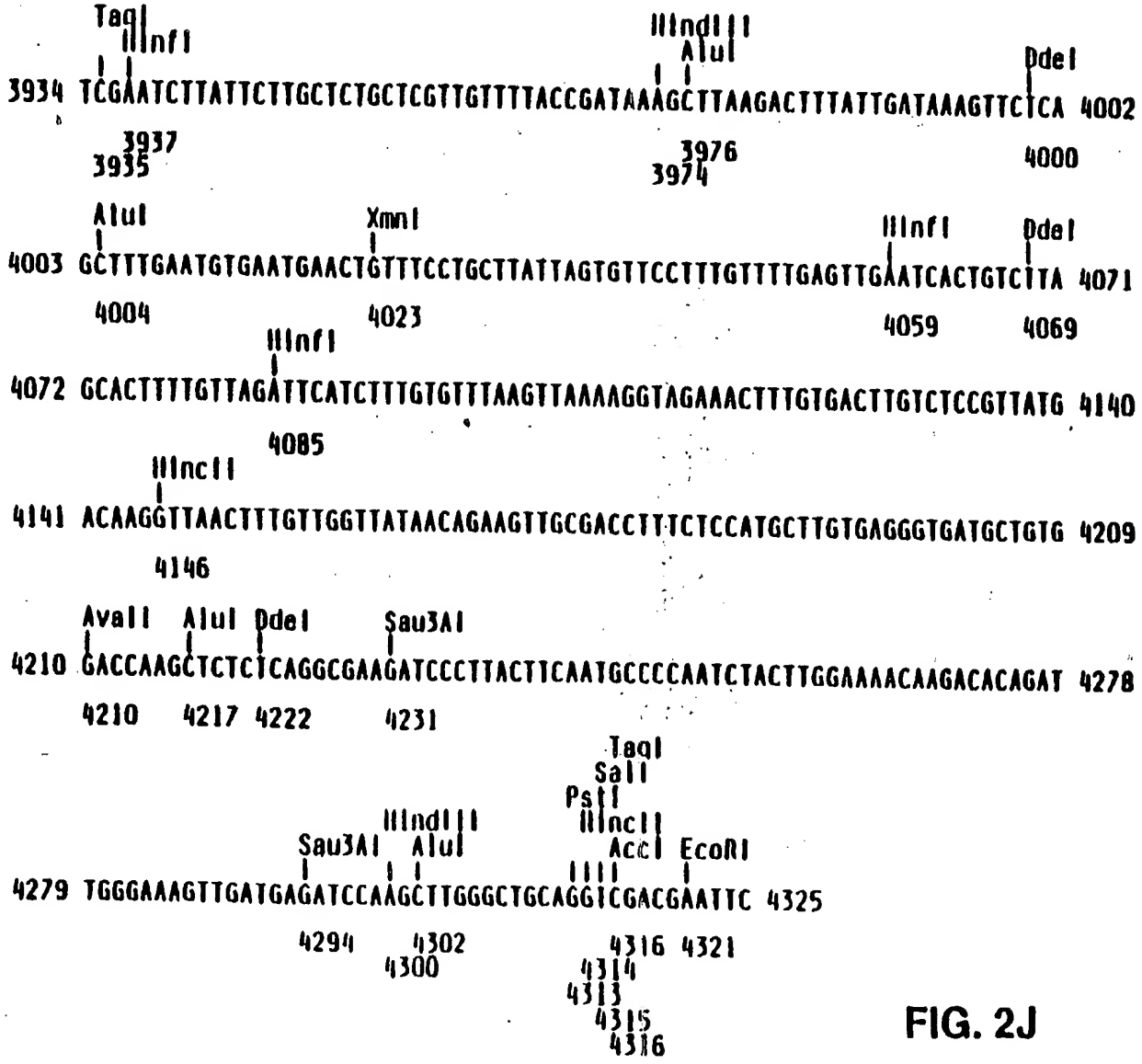

TaqI
HinfI
HindIII
AluI
PdeI
3934 TCGAATCTTATTCTTGCTCTGCTCGTTGTTTTACCGATAAAGCTTAAGACTTTATTGATAAAGTTCTCA 4002
3937
3935
3976
3974
4000
AluI
XmnI
HinfI
PdeI
4003 GCTTTGAATGTGAATGAACTGTTTCCTGCTTATTAGTGTTCCTTTGTTTTGAGTTGAATCACTGTCTTA 4071
4004
4023
4059
4069
HinfI
4072 GCACTTTTGTTAGATTCATCTTTGTGTTTAAGTTAAAAGGTAGAAACTTTGTGACTTGTCTCCGTTATG 4140
4085
HincII
4141 ACAAGGTTAACTTTGTTGGTTATAACAGAAGTTGCGACCTTTCTCCATGCTTGTGAGGGTGATGCTGTG 4209
4146
AvaII
AluI
PdeI
Sau3AI
4210 GACCAAGCTCTCTCAGGCGAAGATCCCTTACTTCAATGCCCCAATCTACTTGGAAAACAAGACACAGAT 4278
4210
4217
4222
4231
TaqI
SalI
PstI
HindIII
HincII
Sau3AI
AluI
AccI
EcoRI
4279 TGGGAAAGTTGATGAGATCCAAGCTTGGGCTGCAGGTCGACGAATTC 4325
4294
4302
4300
4316
4321
4314
4313
4315
4316

FIG. 2J

Brassica campestris ACP Genomic Sequence

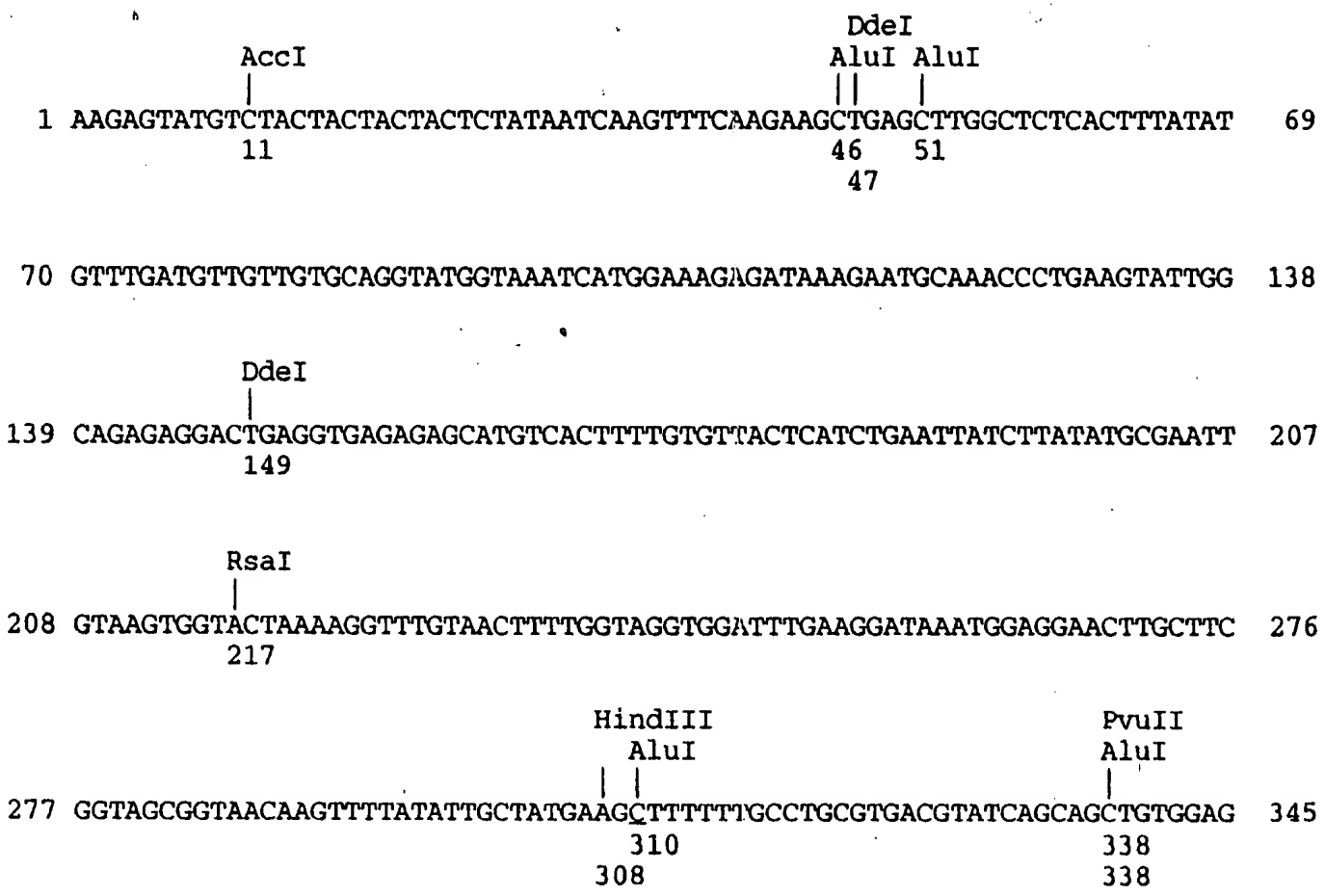


FIG. 3A

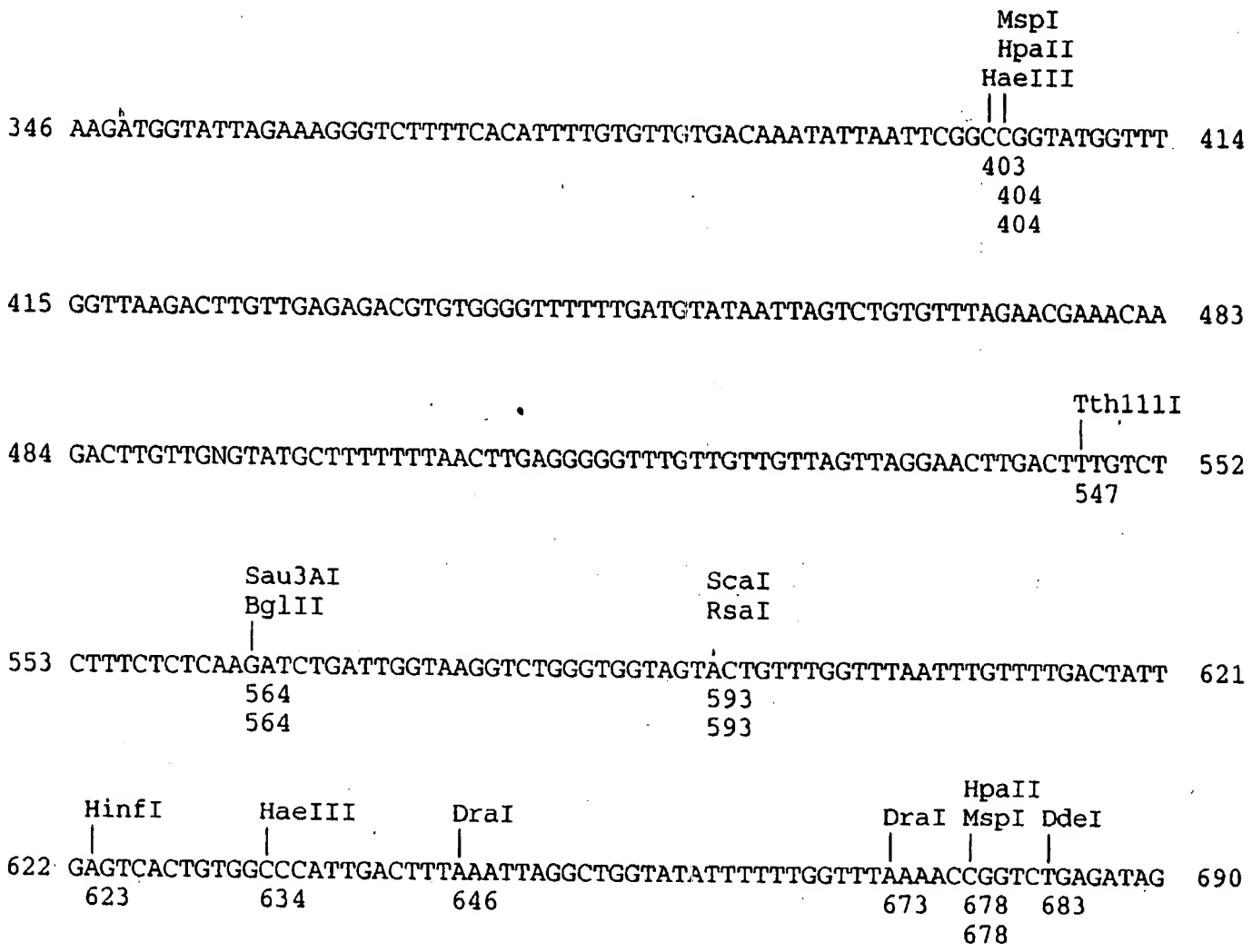

MspI
HpaII
HaeIII
346 AAGATGGTATTAGAAAGGGTCTTTTCACATTTTGTGTTGTGACAAATATTAATTCGGCCGGTATGGTTT 414
403
404
404
415 GGTTAAGACTTGTTGAGAGACGTGTGGGGTTTTTTGATGTATAATTAGTCTGTGTTTAGAACGAAACAA 483
Tth111I
484 GACTTGTTGNGTATGCTTTTTTTAACTTGAGGGGGTTTGTTGTTGTTAGTTAGGAACTTGACTTTGTCT 552
547
Sau3AI
BglII
ScaI
RsaI
553 CTTTCTCTCAAGATCTGATTGGTAAGGTCTGGGTGGTAGTACTGTTTGGTTTAATTTGTTTTGACTATT 621
564
564
593
593
HinfI
HaeIII
DraI
HpaII
DraI MspI DdeI
622 GAGTCACTGTGGCCCATTGACTTTAAATTAGGCTGGTATATTTTTTGGTTTAAAACCGGTCTGAGATAG 690
623
634
646
673
678
683
678

FIG. 3B

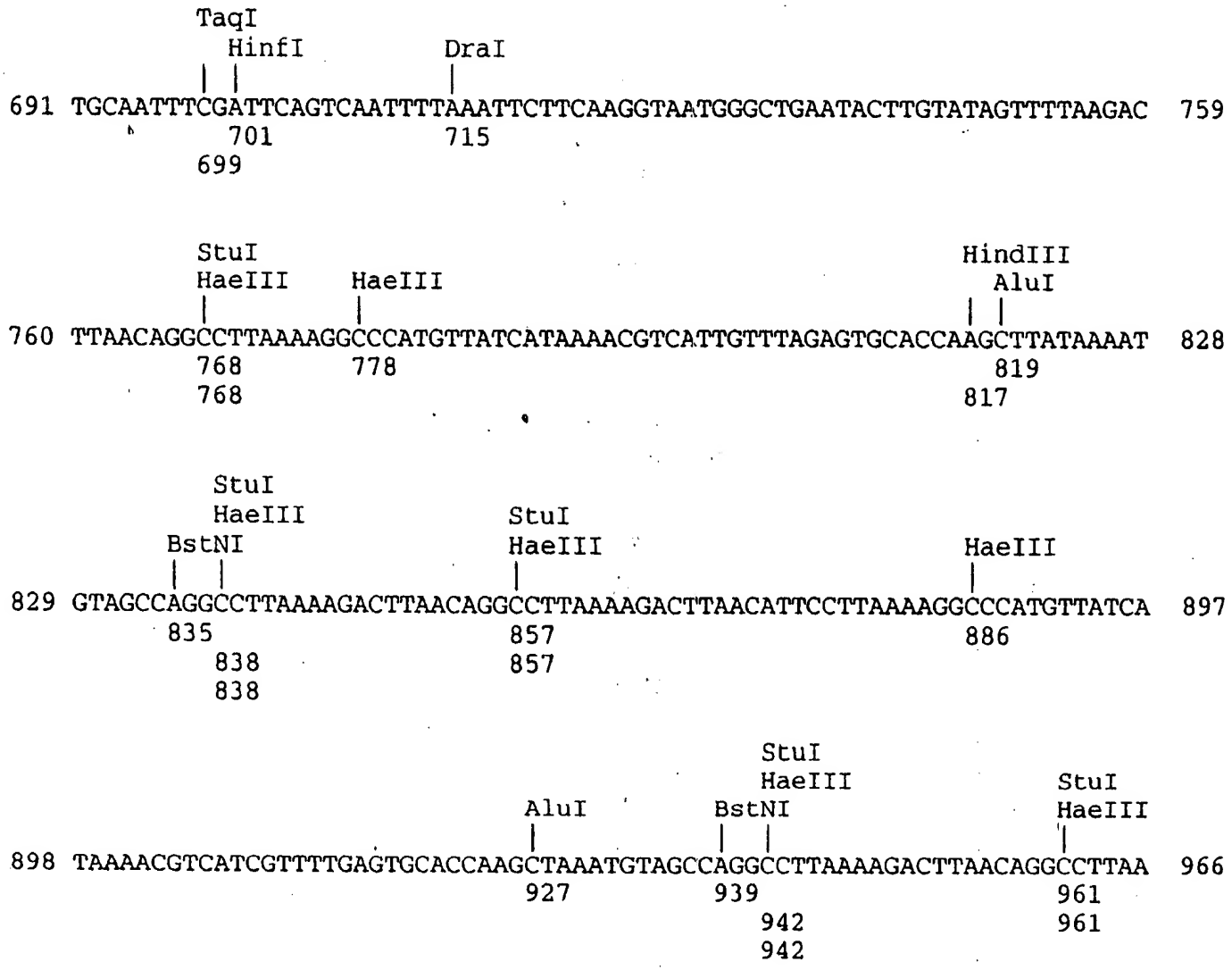

TaqI
HinfI
DraI
691 TGCAATTTCGATTCAGTCAATTTTAAATTCTTCAAGGTAATGGGCTGAATACTTGTATAGTTTTAAGAC 759
701
715
699
StuI
HaeIII
HaeIII
HindIII
AluI
760 TTAACAGGCCTTAAAAGGCCCATGTTATCATAAAACGTCATTGTTTAGAGTGCACCAAGCTTATAAAAT 828
768
778
819
768
817
StuI
HaeIII
StuI
HaeIII
BstNI
HaeIII
829 GTAGCCAGGCCTTAAAAGACTTAACAGGCCTTAAAAGACTTAACATTCCTTAAAAGGCCCATGTTATCA 897
835
857
886
838
857
838
StuI
HaeIII
StuI
HaeIII
AluI
BstNI
898 TAAAACGTCATCGTTTTGAGTGCACCAAGCTAAATGTAGCCAGGCCTTAAAAGACTTAACAGGCCTTAA 966
927
939
961
942
961
942

FIG. 3C

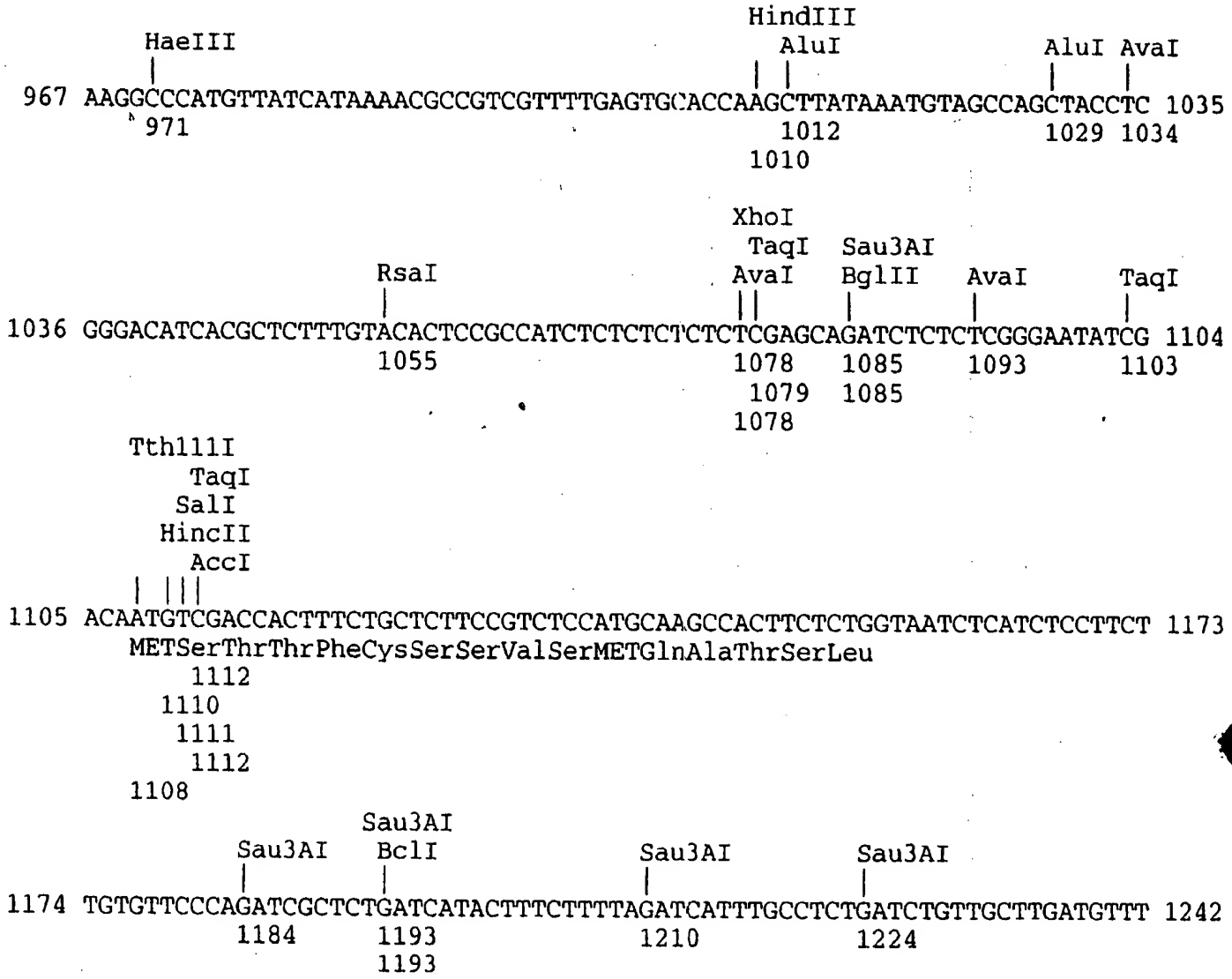

HaeIII
HindIII
AluI
AluI AvaI
967 AAGGCCCATGTTATCATAAAACGCCGTCGTTTTGAGTGCACCAAGCTTATAAATGTAGCCAGCTACCTC 1035
971
1012
1029 1034
1010
XhoI
TaqI
Sau3AI
RsaI
AvaI
BglII
AvaI
TaqI
1036 GGGACATCACGCTCTTTGTACACTCCGCCATCTCTCTCTCTCTCGAGCAGATCTCTCTCGGGAATATCG 1104
1055
1078
1085
1093
1103
1079
1085
1078
Tth111I
TaqI
SalI
HincII
AccI
1105 ACAATGTCGACCACTTTCTGCTCTTCCGTCTCCATGCAAGCCACTTCTCTGGTAATCTCATCTCCTTCT 1173
METSerThrThrPheCysSerSerValSerMETGlnAlaThrSerLeu
1112
1110
1111
1112
1108
Sau3AI
Sau3AI
BclI
Sau3AI
Sau3AI
1174 TGTGTTCCCAGATCGCTCTGATCATACTTTCTTTTAGATCATTTGCCTCTGATCTGTTGCTTGATGTTT 1242
1184
1193
1210
1224
1193

FIG. 3D

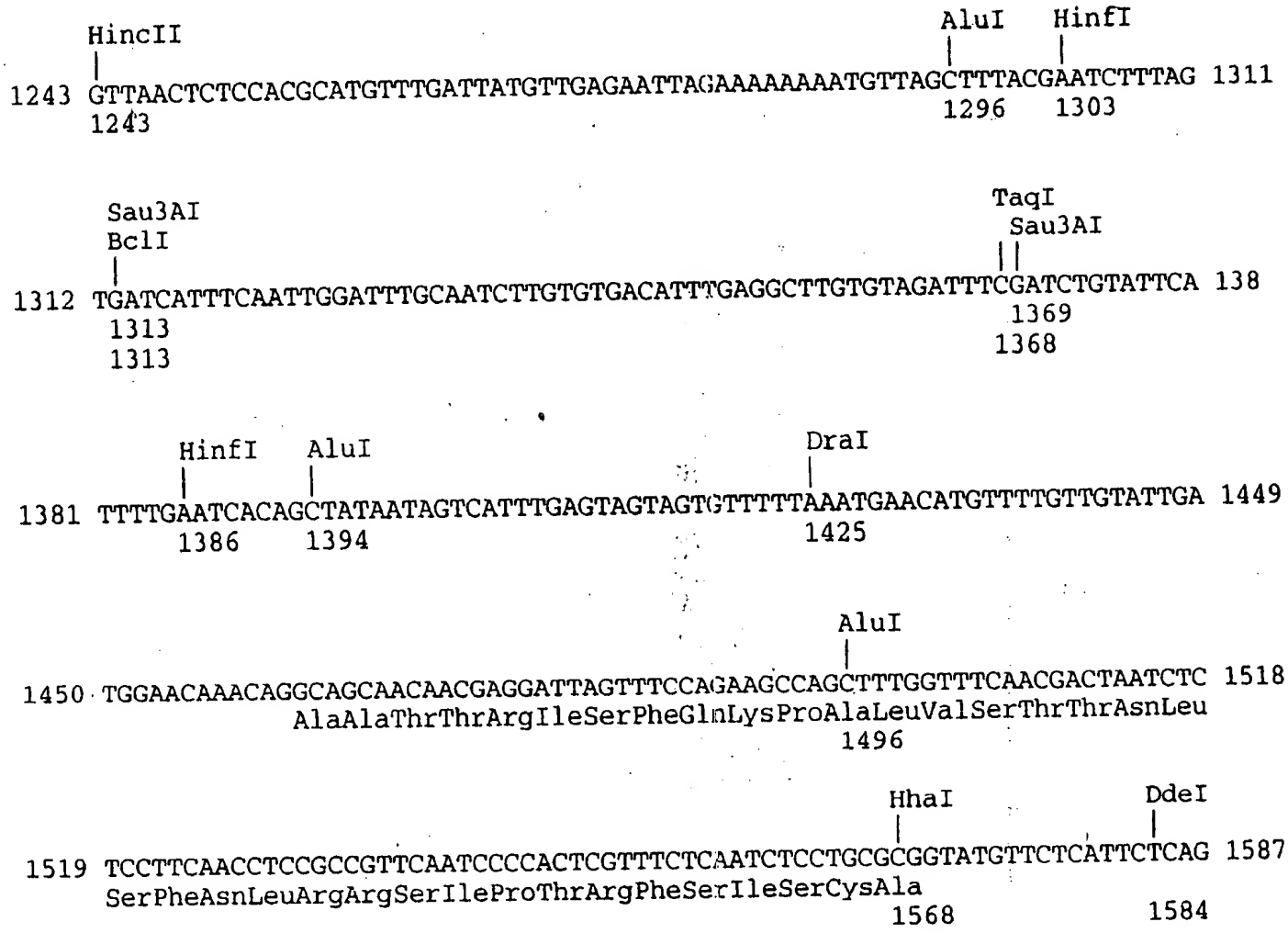

HincII
AluI
HinfI
1243 GTTAACTCTCCACGCATGTTTGATTATGTTGAGAATTAGAAAAAAAATGTTAGCTTTACGAATCTTTAG 1311
1243
1296
1303
Sau3AI
BclI
TaqI
Sau3AI
1312 TGATCATTTCAATTGGATTTGCAATCTTGTGTGACATTTGAGGCTTGTGTAGATTTCGATCTGTATTCA 138
1313
1313
1369
1368
HinfI
AluI
DraI
1381 TTTTGAATCACAGCTATAATAGTCATTTGAGTAGTAGTGTTTTTAAATGAACATGTTTTGTTGTATTGA 1449
1386
1394
1425
AluI
1450 TGGAACAAACAGGCAGCAACAACGAGGATTAGTTTCCAGAAGCCAGCTTTGGTTTCAACGACTAATCTC 1518
AlaAlaThrThrArgIleSerPheGlnLysProAlaLeuValSerThrThrAsnLeu
1496
HhaI
DdeI
1519 TCCTTCAACCTCCGCCGTTCAATCCCCACTCGTTTCTCAATCTCCTGCGCGGTATGTTCTCATTCTCAG 1587
SerPheAsnLeuArgArgSerIleProThrArgPheSerIleSerCysAla
1568
1584

FIG. 3E

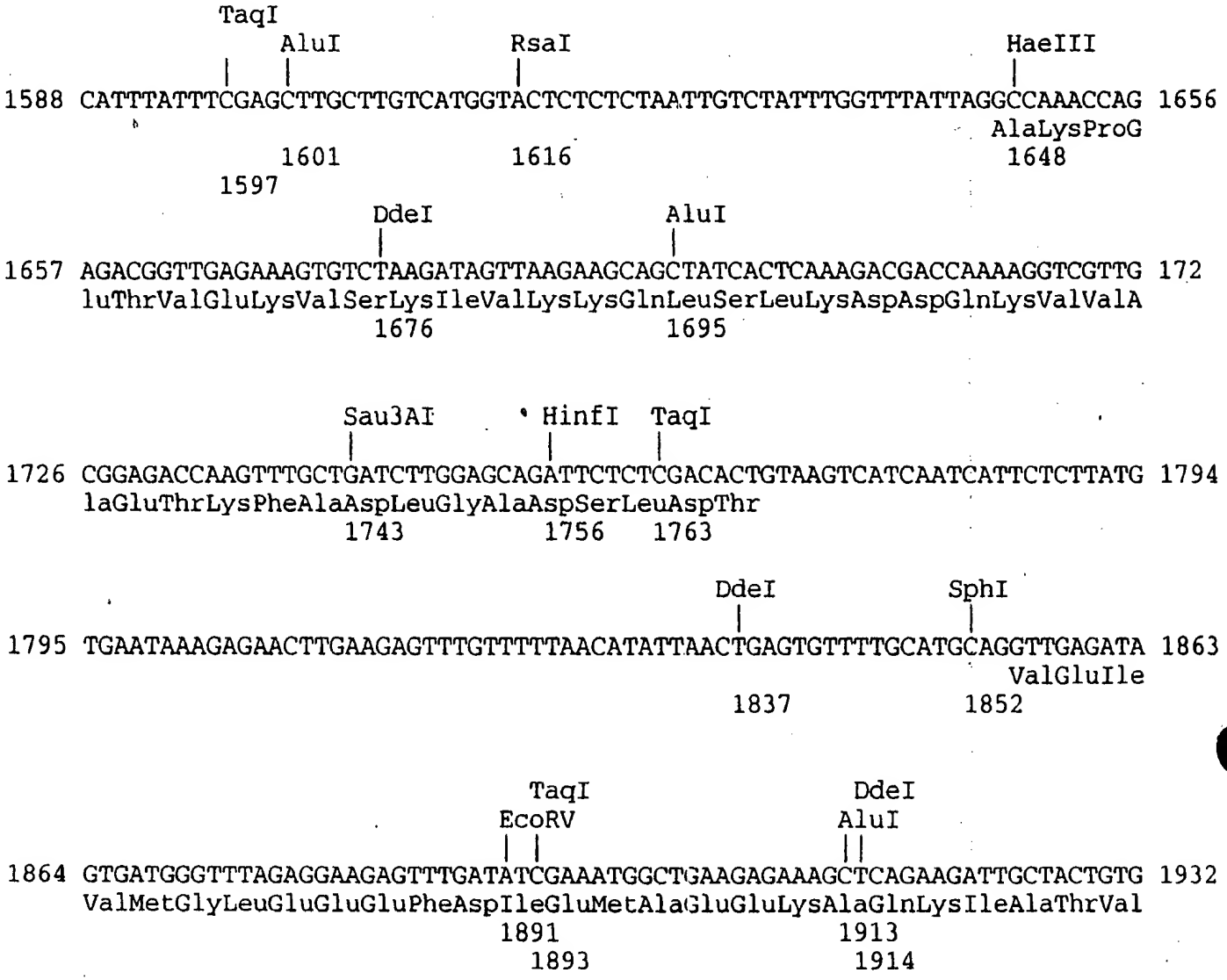

TaqI
AluI
RsaI
HaeIII
1588 CATTTATTTCGAGCTTGCTTGTCATGGTACTCTCTCTAATTGTCTATTTGGTTTATTAGGCCAAACCAG 1656
AlaLysProG
1601
1616
1648
1597
DdeI
AluI
1657 AGACGGTTGAGAAAGTGTCTAAGATAGTTAAGAAGCAGCTATCACTCAAAGACGACCAAAAGGTCGTTG 172
luThrValGluLysValSerLysIleValLysLysGlnLeuSerLeuLysAspAspGlnLysValValA
1676
1695
Sau3AI
HinfI
TaqI
1726 CGGAGACCAAGTTTGCTGATCTTGGAGCAGATTCTCTCGACACTGTAAGTCATCAATCATTCTCTTATG 1794
laGluThrLysPheAlaAspLeuGlyAlaAspSerLeuAspThr
1743
1756
1763
DdeI
SphI
1795 TGAATAAAGAGAACTTGAAGAGTTTGTTTTTAACATATTAACTGAGTGTTTTGCATGCAGGTTGAGATA 1863
ValGluIle
1837
1852
TaqI
EcoRV
DdeI
AluI
1864 GTGATGGGTTTAGAGGAAGAGTTTGATATCGAAATGGCTGAAGAGAAAGCTCAGAAGATTGCTACTGTG 1932
ValMetGlyLeuGluGluGluPheAspIleGluMetAlaGluGluLysAlaGlnLysIleAlaThrVal
1891
1893
1913
1914

FIG. 3F

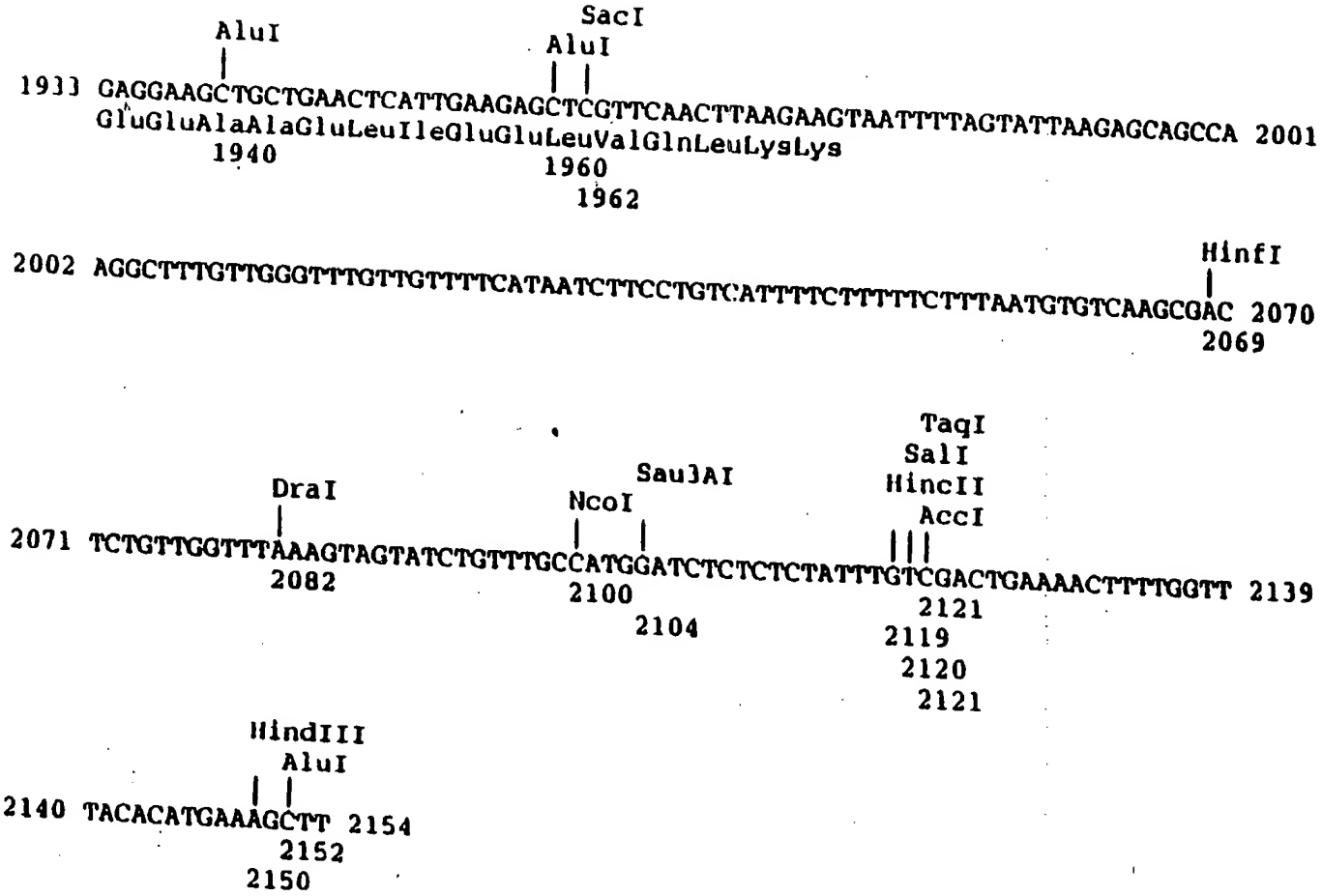
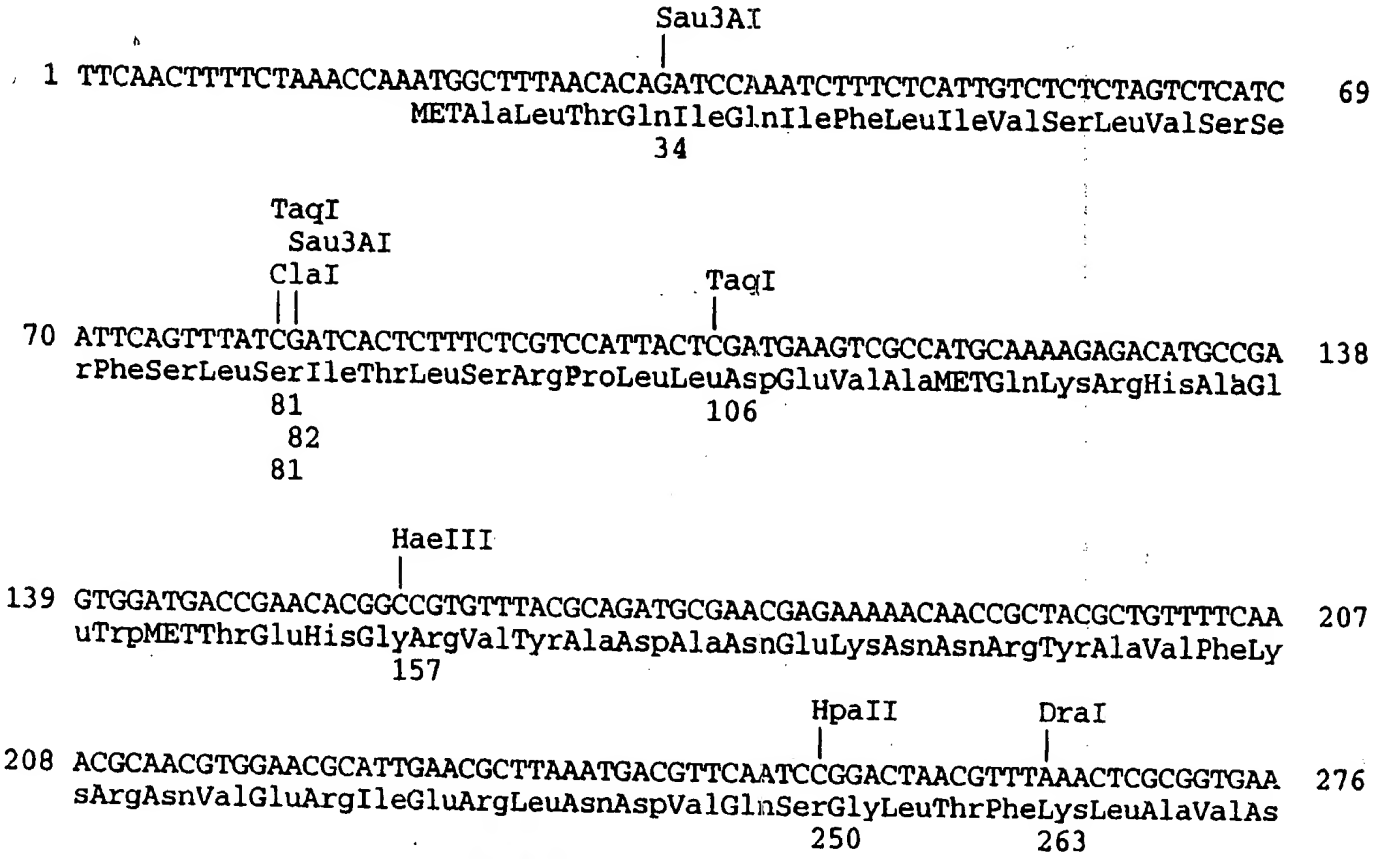

AluI
SacI
AluI
1933 GAGGAAGCTGCTGAACTCATTGAAGAGCTCGTTCAACTTAAGAAGTAATTTTAGTATTAAGAGCAGCCA 2001
GluGluAlaAlaGluLeuIleGluGluLeuValGlnLeuLysLys
1940
1960
1962
HinfI
2002 AGGCTTTGTTGGGTTTGTTGTTTTCATAATCTTCCTGTCATTTTCTTTTTCTTTAATGTGTCAAGCGAC 2070
2069
TaqI
SalI
Sau3AI
DraI
NcoI
HincII
AccI
2071 TCTGTTGGTTTAAAGTAGTATCTGTTTGCCATGGATCTCTCTCTATTTGTCGACTGAAAACTTTTGGTT 2139
2082
2100
2104
2121
2119
2120
2121
HindIII
AluI
2140 TACACATGAAAGCTT 2154
2152
2150

FIG. 3G

Brassica Campestris Seed Specific cDNA-EA9



Complete nucleotide sequence of B. campestris cDNA EA9. The longest open reading frame is designated by three letter amino acid code. PolyA tails are evident at the end of th sequence and a potential polyadenylation signal is underlined.

FIG. 4A

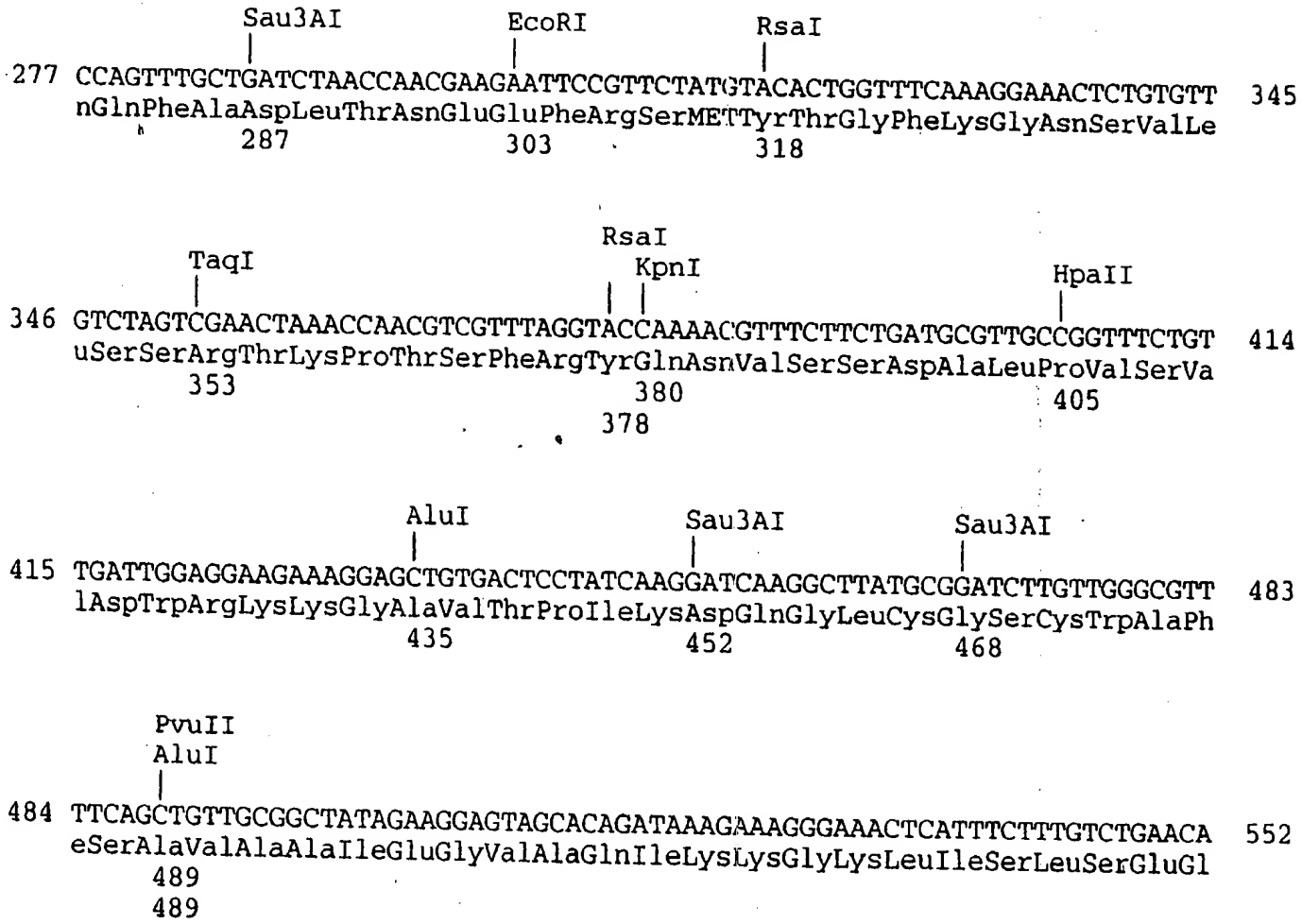

Sau3AI
EcoRI
RsaI
277 CCAGTTTGCTGATCTAACCAACGAAGAATTCCGTTCTATGTACACTGGTTTCAAAGGAAACTCTGTGTT 345
nGlnPheAlaAspLeuThrAsnGluGluPheArgSerMETTyrThrGlyPheLysGlyAsnSerValLe
287
303
318
RsaI
TaqI
KpnI
HpaII
346 GTCTAGTCGAACTAAACCAACGTCGTTTAGGTACCAAAACGTTTCTTCTGATGCGTTGCCGGTTTCTGT 414
uSerSerArgThrLysProThrSerPheArgTyrGlnAsnValSerSerAspAlaLeuProValSerVa
353
380
405
378
AluI
Sau3AI
Sau3AI
415 TGATTGGAGGAAGAAAGGAGCTGTGACTCCTATCAAGGATCAAGGCTTATGCGGATCTTGTTGGGCGTT 483
lAspTrpArgLysLysGlyAlaValThrProIleLysAspGlnGlyLeuCysGlySerCysTrpAlaPh
435
452
468
PvuII
AluI
484 TTCAGCTGTTGCGGCTATAGAAGGAGTAGCACAGATAAAGAAAGGGAAACTCATTTCTTTGTCTGAACA 552
eSerAlaValAlaAlaIleGluGlyValAlaGlnIleLysLysGlyLysLeuIleSerLeuSerGluGl
489
489

FIG. 4B

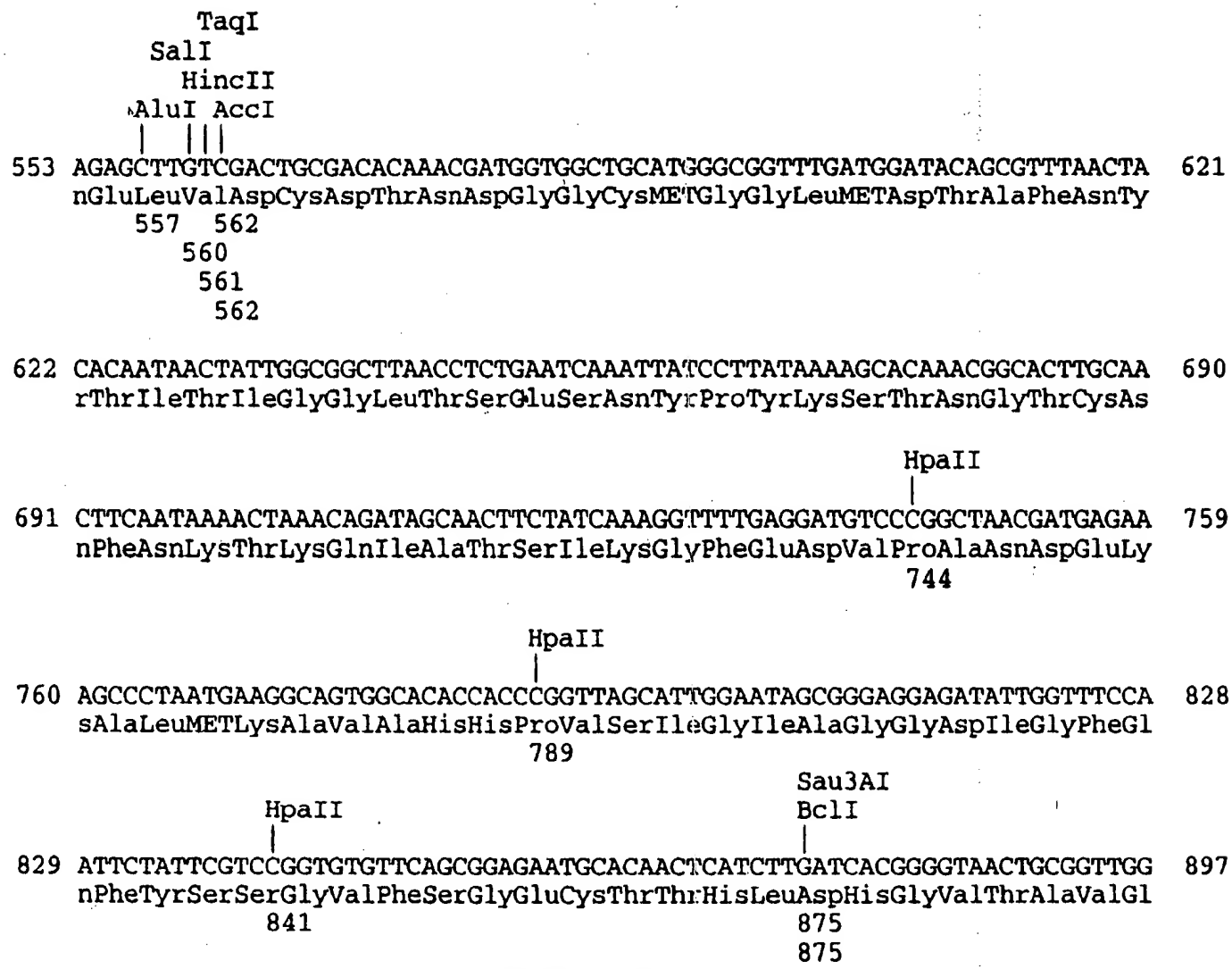

TaqI
SalI
HincII
AluI AccI
553 AGAGCTTGTCGACTGCGACACAAACGATGGTGGCTGCATGGGCGGTTTGATGGATACAGCGTTTAACTA 621
nGluLeuValAspCysAspThrAsnAspGlyGlyCysMETGlyGlyLeuMETAspThrAlaPheAsnTy
557 562
560
561
562
622 CACAATAACTATTGGCGGCTTAACCTCTGAATCAAATTATCCTTATAAAAGCACAAACGGCACTTGCAA 690
rThrIleThrIleGlyGlyLeuThrSerGluSerAsnTyrProTyrLysSerThrAsnGlyThrCysAs
HpaII
691 CTTCAATAAAACTAAACAGATAGCAACTTCTATCAAAGGTTTTGAGGATGTCCCGGCTAACGATGAGAA 759
nPheAsnLysThrLysGlnIleAlaThrSerIleLysGlyPheGluAspValProAlaAsnAspGluLy
744
HpaII
760 AGCCCTAATGAAGGCAGTGGCACACCACCCGGTTAGCATTGGAATAGCGGGAGGAGATATTGGTTTCCA 828
sAlaLeuMETLysAlaValAlaHisHisProValSerIleGlyIleAlaGlyGlyAspIleGlyPheGl
789
Sau3AI
HpaII BclI
829 ATTCTATTCGTCCGGTGTGTTCAGCGGAGAATGCACAACTCATCTTGATCACGGGGTAACTGCGGTTGG 897
nPheTyrSerSerGlyValPheSerGlyGluCysThrThrHisLeuAspHisGlyValThrAlaValGl
841
875
875

FIG. 4C

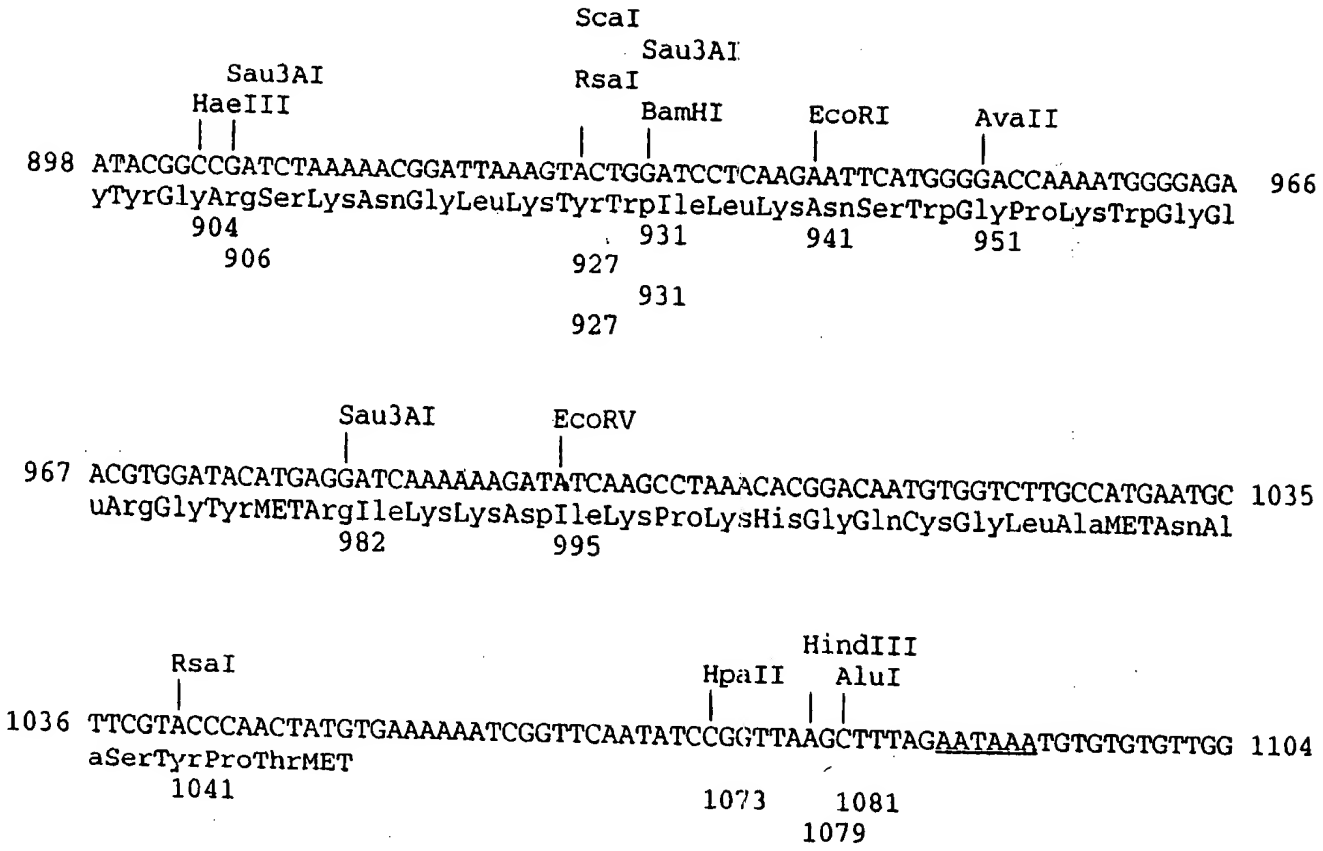

ScaI
Sau3AI
Sau3AI
RsaI
HaeIII
BamHI
EcoRI
AvaII
898 ATACGGCCGATCTAAAAACGGATTAAAGTACTGGATCCTCAAGAATTCATGGGGACCAAAATGGGGAGA 966
yTyrGlyArgSerLysAsnGlyLeuLysTyrTrpIleLeuLysAsnSerTrpGlyProLysTrpGlyGl
904
906
931
941
951
927
931
927
Sau3AI
EcoRV
967 ACGTGGATACATGAGGATCAAAAAAGATATCAAGCCTAAACACGGACAATGTGGTCTTGCCATGAATGC 1035
uArgGlyTyrMETArgIleLysLysAspIleLysProLysHisGlyGlnCysGlyLeuAlaMETAsnAl
982
995
RsaI
HindIII
HpaII
AluI
1036 TTCGTACCCAACTATGTGAAAAAATCGGTTCAATATCCGGTTAAGCTTTAGAATAAATGTGTGTGTTGG 1104
aSerTyrProThrMET
1041
1073
1081
1079
1105 TTATAATTTAAGACTCTGTTGCATGTAATTTGTGAAATGGTAAGTTTATGTGATGCAAAAGATTTGATA 1173
1174 AAAAAAAAAAAAA 1186

FIG. 4D

```
3H11 TTTTTTTGAGCAAAGGGCAACTCAGATATCCAAAGATGAATCCAACATATA 51

3H11 GCTTACAGCTGGGAGAACATTGTCTAACTCTTCTGAAATTTAAATGTTATC 102

3H11 CAGAATCCTTCATCATAAAATAATATCAAAATGCAAATCTATTTTTTCTAC 153

3H11 TCTTGTCTAGCTTCAACTTTCTTCTTCTGCTCATCAATTAGCAATTAATCC 204
                                    TGCTCATCAATTAGCAATTAATCC

3H11 AAAACCATTATGGCTGCCAAAAATTCAGAGATGAAGTTTGCTATCTTCTTC 255
2A11 AAAACCATTATGGCTGCCAAAAATTCAGAGATGAAGTTTGCTATCTTCTTC
              METAlaAlaLysAsnSerGluMETLysPheAlaIlePhePhe

3H11 GTTGTTCTTTTGACGACCACTTTAGTTGATATGTCTGGAATTTCGAAAATG 306
2A11 GTTGTTCTTTTGACGACCACTTTAGTTGATATGTCTGGAATTTCGAAAATG
     ValValLeuLeuThrThrThrLeuValAspMETSerGlyIleSerLysMET

3H11 CAAGTGATGGCTCTTCGAGACATACCCCCACAAGAAACATTGCTGAAAATG 357
2A11 CAAGTGATGGCTCTTCGAGACATACCCCCACAAGAAACATTGCTGAAAATG
     GlnValMETAlaLeuArgAspIleProProGlnGluThrLeuLeuLysMET

3H11 AAGCTACTTCCCACAAATATTTTGGGACTTTGTAACGAACCTTGCAGCTCA 408
2A11 AAGCTACTTCCCACAAATATTTTGGGACTTTGTAACGAACCTTGCAGCTCA
     LysLeuLeuProThrAsnIleLeuGlyLeuCysAsnGluProCysSerSer

3H11 AACTCTGATTGCATCGGAATTACCCTTTGCCAATTTTGTAAGGAGAAGACG 459
2A11 AACTCTGATTGCATCGGAATTACCCTTTGCCAATTTTGTAAGGAGAAGACG
     AsnSerAspCysIleGlyIleThrLeuCysGlnPheCysLysGluLysThr

3H11 GACCAGTATGGTTTAACATACCGTACATGCAACCTGTTGCCTTGAACAATA 510
2A11 GACCAGTATGGTTTAACATACCGTACATGCAACCTGTTGCCTTGAACAATA
     AspGlnTyrGlyLeuThrTyrArgThrCysAsnLeuLeuPro .
```

FIGURE 5A

```
3H11 TCAATGATCTATCGATCGATCTATCTATCTATTTATCTGTCTCTGCGCGTA 561
2A11 TCAATGATCTATCGATCGATCTATCTATCTATTTATCTGTCTCTGCGCGTA

3H11 TAGTGTTGTCTGTACCTTTGGTGTGAAGAATATGAATAAAGGGATACATAT 612
2A11 TAGTGTTGTCTGTACCTTTGGTGTGAAGAATATGAATAAAGGGATACATAT

3H11 ATCTAGATATATTCTAGGTAATGTCCTATTGTATTTAAAATTTGTAGCAAT 663
2A11 ATCTAGATATATTCTAGGTAATGTCCTATTGTATTTAAAATTTGTAGCAAT

3H11 GATTGTTTGAATAAAAACATACCATGAGTGAAATAATTATTCCACATTAAT 714
2A11 GATTGTTTGAATAAAAACATACCATGAGTGAAATAATTATTCC

3H11 TCACGTATTTATTTCACTTATGATACGTATTTTTGTTCCTTTCGCGTAAAA 765

3H11 AAAAAAAAA     774
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FIGURE 5B

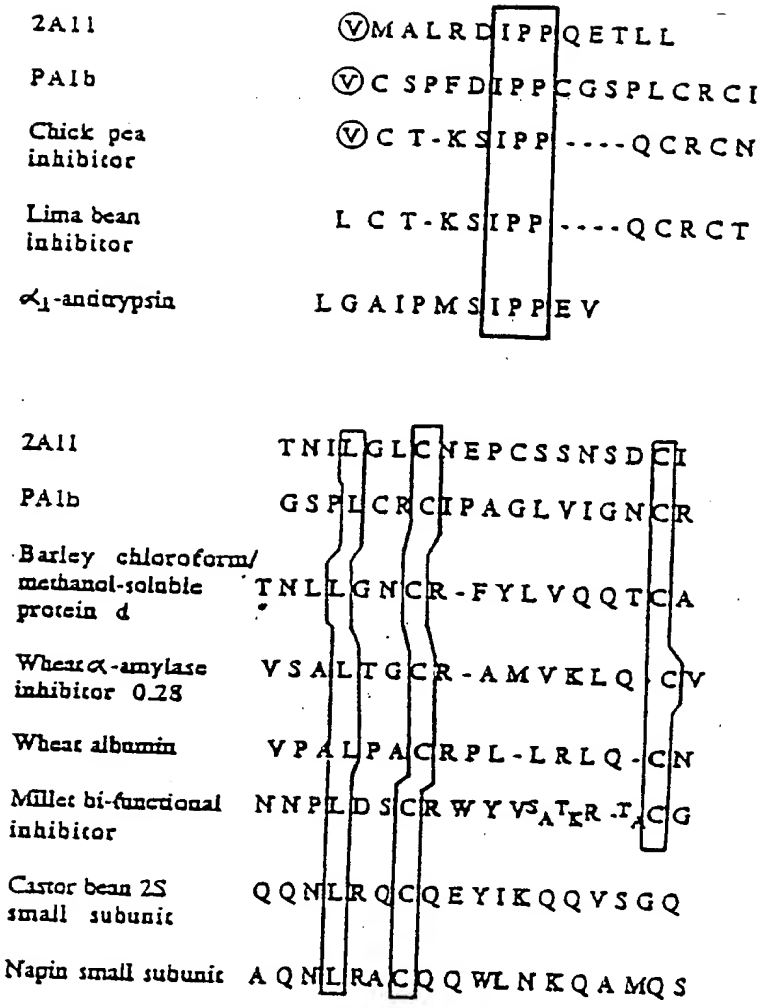
2A11
ⓋMALRDIPPQETLL
PA1b
ⓋCSPFDIPPCGSPLCRCI
Chick pea inhibitor
ⓋCT-KSIPP----QCRCN
Lima bean inhibitor
LCT-KSIPP----QCRCT
α1-antitrypsin
LGAIPMSIPPEV
2A11
TNILGLCNEPCSSNSDCI
PA1b
GSPLCRCIPAGLVIGNCR
Barley chloroform/ methanol-soluble protein d
TNLLGNCR-FYLVQQTCA
Wheat α-amylase inhibitor 0.28
VSALTGCR-AMVKLQCV
Wheat albumin
VPALPACRPL-LRLQ-CN
Millet bi-functional inhibitor
NNPLDSCRWYVSATERTACG
Castor bean 2S small subunit
QQNLRQCQEYIKQQVSGQ
Napin small subunit
AQNLRACQQWLNKQAMQS

FIGURE 6

2A11 GENOMIC

```
        10          20          30          40          50
CTCGAGCCCT TTAAAAAGTA TAGTCAATAT TTACGGTGAC CGTGAATTTC
        60          70          80          90         100
TTAATTATGA TATATAATTT AAAAGAAATC ATGATCACAT TCTACTGATG
       110         120         130         140         150
AGAACATGTG CTAATCAAGG GAAAACATGG ATGTGAAAAA TACTTTTTGT
       160         170         180         190         200
TAAAAGTAAA AAAAAATGTG AAATTTTGTT AGTTATTTAC TACCTATACA
       210         220         230         240         250
TTATTTGAGC ATGTGCAAAC TTTACAAATA CCTAATAGAA GATTTTCACC
       260         270         280         290         300
TGCCTGTATA TATGTAAATT AATTATAATG AACACTCTCA CATAAAATAA
       310         320         330         340         350
TTATCAGTAT ATACATTAAT ACTTGCCCTC CACAATGAAT TAAATAAAAT
       360         370         380         390         400
GTAGAACATG ATCTACACTT CAATAAAACT AAGACCATAA AGAATAATTT
       410         420         430         440         450
CAAAATATAC ACATGTCAAC AATAAATTAT TTGCATATTA TATTAACTTA
       460         470         480         490         500
CTAAACAATC TTTACTTTTG AAATATAAAA ATAATCAAGT TATAAGTCTG
       510         520         530         540         550
CTCAAAGTAA AGCACTTGTT AGACTCATCT GATTTTGAGA AGGTAAGCAA
       560         570         580         590         600
ATTGATGGTG CATAATAGTC ACAAGTAAAA TATAAAATAG ATTTCATTAG
       610         620         630         640         650
TAAAATTGTT TTTTACTTTC TTTATATATA ATTATCAATA TCCTTCAATG
       660         670         680         690         700
GTAGGTTAAT TATATTGTTA ACTTCTTGTT GAATTAAAGC AATAAGACAA
       710         720         730         740         750
GAATATTAAA GATAAAAGAA CAATAAAAAT AGAAAGACTA AGAGATAAGA
       760         770         780         790         800
GTTTTCTTAT TCTTCTTTCA ATAAGTATCA TCAAGTGTAT ACAATATAAA
       810         820         830         840         850
TTTTTGTATT TTTGATCTAT CTATTTATAA TGTTATATAT AAGCATACAA
       860         870         880         890         900
AAGATCAGTC ATAAATATGA CTTTAATCAT GAAAATAATG AAAGAGATTA
       910         920         930         940         950
TGAAGGCGTA AGGTTACTAG AATAATAGTC ATTAAAAAAA GGGGTTATCT
       960         970         980         990        1000
TTATAATTGA ATAATTGATG AAGTAATGGA GATAATTAGT GAGCATAAAT
      1010        1020        1030        1040        1050
TTTTTTAAAA AAATGGACAT TTACACTATA ATATTTTATA ACACTTTCCC
      1060        1070        1080        1090        1100
TTAAACATCT AGGTATAAAT AATGAGTCTT GTCAAAATCT TAGTAGGAAA
```

FIGURE 7A

```
    1110        1120        1130        1140        1150
 AATTCTGTGA AATTTTTTTA GTGAAAACAA ATGATATAAA TATCTTGAAT
       1160        1170        1180        1190        1200
 ACTCATTATT TGTTGTCTCA TTAAAAATCT TATCTGACCT ATAAAATAAA
       1210        1220        1230        1240        1250
 TTATTTGCTC AACTCAAAAT AGTTTTTCAT TCTAAAATTA GTATAATTAT
       1260        1270        1280        1290        1300
 TAGTGAATAT TTAATTAACA TAATTGTATA CTAAGGGGCC TATAAATTGG
       1310        1320        1330        1340        1350
 ATTCTTCTCA AAGAAAAATA AAATCACCAC ACAACTTTCT TCTTCTGCTC
       1360        1370          1381        1390
 ATCAATTAGC AATTAATCCA AAACCATT ATG GCT GCC AAA AAT
                                  MET Ala Ala Lys Asn
    1399        1408        1417        1426
 TCA GAG ATG AAG TTT GCT ATC TTC TTC GTT GTT CTT TTG
 Ser Glu MET Lys Phe Ala Ile Phe Phe Val Val Leu Leu
1435        1444        1454        1464        1474
 ACG ACC ACT TTA GGTTCACAAC ACTTCTCCCT TATTTTGTTT
 Thr Thr Thr Leu
       1484        1494        1504        1514        1524
 TCTTAATTTC TTGGAAGTCA TATGCATGTG TTTGGTATCA TGGTATATAT
       1534        1544        1554        1564        1574
 ATAAAGGAAA ATATTTTTCT TAATTACTGG TTTTCTAATG TTTGGTAGGT
       1584        1594        1604        1614        1624
 AATCGGAAAT TATTATGAGA TAATGAACTT GCAAAGTCAT TATTATATAA
       1634        1644        1654        1664        1674
 CTTTTTTTTT ATACTTTGAT TTAAGAATTC ATTTTTCTCA TTTTATATAA
       1684        1694        1704        1714        1724
 ACTTATTTTT CAACAGAAAA TATTTTTCGA ACTATTCAAA CACACCCTAA
       1734        1744        1754        1764        1774
 GACATTACAT ATATATATAT ATACACCCTC CGTTTTATAT TACTTAATGC
       1784        1794        1804        1814        1824
 CTATTGAGTT GGCCCACCCT TTAAGAATGA TTCAATTAGA GATATGTTTT
       1834        1844        1854        1864        1874
 ACTAAATTAA CCTATGCTTT AAGACTCTAA ATTTGGCTAT TACTATTTTA
       1884        1894        1904        1914        1924
 CGTTGTAATT TAATGACAAA CATTTCATAA TGACTATAGT CTGAACTTAA
       1934        1944        1954        1964        1974
 TTAGACAGAC GTATCTATAG TTTGCTTACT AATGATTCAT AGCTATATAT
       1984        1994        2004        2014        2024
 TTGGAGAGGA GAGAGACAAA CGATATTAAG AAAGGGAGGA GAGAGGCGAG
       2034        2044        2054        2064        2074
 GTAAATCTGA AATAGAGAAG AGAAAGGCAA CCAATTTTGA TCATCTATCA
       2084        2094        2104        2114        2124
 TACTTTTGAT TATTATTTTT ATTATATGTA CGTTTACATT ACAGTTTTCG
```

FIGURE 7B

```
     2134        2144        2154         2164
AATTCTTACA TTAATCTTAA TCATAATATA TACA GTT GAT ATG
                                      Val Asp MET

   2173        2182        2191        2200
TCT GGA ATT TCG AAA ATG CAA GTG ATG GCT CTT CGA GAC
Ser Gly Ile Ser Lys MET Gln Val MET Ala Leu Arg Asp
2209        2218        2227        2236        2245
ATA CCC CCA CAA GAA ACA TTG CTG AAA ATG AAG CTA CTT
Ile Pro Pro Gln Glu Thr Leu Leu Lys MET Lys Leu Leu
       2254        2263        2272        2281
CCC ACA AAT ATT TTG GGA CTT TGT AAC GAA CCT TGC AGC
Pro Thr Asn Ile Leu Gly Leu Cys Asn Glu Pro Cys Ser
   2290        2299        2308        2317
TCA AAC TCT GAT TGC ATC GGA ATT ACC CTT TGC CAA TTT
Ser Asn Ser Asp Cys Ile Gly Ile Thr Leu Cys Gln Phe
2326        2335        2344        2353        2362
TGT AAG GAG AAG ACG GAC CAG TAT GGT TTA ACA TAC CGT
Cys Lys Glu Lys Thr Asp Gln Tyr Gly Leu Thr Tyr Arg
       2371        2380            2393        2403
ACA TGC AAC CTG TTG CCT TGA ACAATATCAA TGATCTATCG
Thr Cys Asn Leu Leu Pro .
      2413        2423        2433        2443        2453
ATCGATCTAT CTATCTATTT ATCTGTCTCT GCGCGTATAG TGTTGTCTGT
      2463        2473        2483        2493        2503
ACCTTTGGTG TGAAGAATAT GAATAAAGGG ATACATATAT CTAGATATAT
      2513        2523        2533        2543        2553
TCTAGGTAAT GTCCTATTGT ATTTAAAATT TGTAGCAATG ATTGTTTGAA
      2563        2573        2583        2593        2603
TAAAAACATA CCATGAGTGA AATAATTATT CCACATTAAT TCACGTATTT
      2613        2623        2633        2643        2653
ATTTCACTTA TGATACGTAT TTTTGTTCCT TTCGCGTAGA TTTTTGATCC
      2663        2673        2683        2693        2703
TTTTCCCTTT TGAATATTAA ACATTAAACA CAAATAATGT TTATTAAATT
      2713        2723        2733        2743        2753
AAGTTAATAT TTTTATTTAG CTATTTATAT TTTTATTTGA AATCAAACTT
      2763        2773        2783        2793        2803
GATAAATATT TATAAAGATA ATTAACAAGT AATGTGACAC TAACACCATG
      2813        2823        2833        2843        2853
TAATATTATC TTGTCGTTAT TTATGATAAT ATTTTAAAAT TATAATTTCA
      2863        2873        2883        2893        2903
GTTAAAAAAT TATTAAAAAA ACATACTTTT AAAAAGTGAG TTAGCCTCCG
      2913        2923        2933        2943        2953
CTACCCACAT ACTTATGAAT TGGACTAGTT GTTTTTTGAC CCACAAAAAG
      2963        2973        2983        2993        3003
AATGGGCTAA TTAAACCTGA CCTATCAAAT TTCAGAATCT GCATAGATTA
```

FIGURE 7C

```
      3013        3023        3033        3043        3053
GTCCGAACGA AATGAGTCAG CCCGTATTGA ACAAAATATC AACAAGGACG
      3063        3073        3083        3093        3103
TTATGTAAAG ATGTTTAAGA AGGAAAAAAG ATTTCTAATA CATATGGACT
      3113        3123        3133        3143        3153
TTCAATATCC CAACTTTGTC TGGCGATCTG AACCCTGCTT AGTTTGTTGA
      3163        3173        3183        3193        3203
TCATTAACTT GTCTTGCTAT GTATTTAAGA TTTAAACTTT ATATGTTTAA
      3213        3223        3233        3243        3253
ACTTACAGAA AATACATATA AATCTCTCAA GACTTGGCAA CATAATTTAC
      3263        3273        3283        3293        3303
TTTAGTACTT AAACTACATG AAAATTTAAA TATCCTTTTA ACATCTTTGA
      3313        3323        3333        3343        3353
AGTGAATTAA ATTATCACAA TCCGAGCCTA CACCTTGGAC GTGGCCGGCA
      3363        3373        3383        3393        3403
CTCAAGAACC AGTGCTGGTC CCCAAGCTAA CCCTCATCCT GACTGACTAC
      3413        3423        3433        3443        3453
AAGCGGAAGG CTAACTTAAG TATACAAAAG CTTAAAACTG AATAAAATAA
      3463        3473        3483        3493        3503
ACTTTACAAG GTTTTAACAC AAATGAACAA CTTTGAAGAA AATAATATAT
      3513        3523        3533        3543        3553
TCAACTAGCC ATAAAATAGA CAACTTTAGT CTTTAAAACA TTTAATAAAA
      3563        3573        3583        3593        3603
TAAATGCAAA ATATAGACTC CTTAACTAAA CTGACTATCT ATGGAGCCTC
      3613        3623        3633        3643        3653
TAATTGATAA AGATGGAAGT CGGGACAAGA CCACGACATC CTGACTAAAC
      3663        3673        3683        3693        3703
TGAGAAGTAA ATAAAATCCC CCGGAAAAAA AGGAGCCTCA CCATGGCTAA
      3713        3723        3733        3743        3753
CTCGAACTCG GGGATATATC AATGAAGCTC CTGTTGATGA TCTTGAAGAC
      3763        3773        3783        3793        3803
ATGTCTCTGC ATCATCAAAA AGATGCAGGC CAAATGGCTC AGTACGTAAA
      3813        3823        3833        3843        3853
ATGTACGAGT ATGTAAGGGA AATTCTAAAG TATAACATAA GCTTGATACT
      3863        3873        3883        3893        3903
TGAATAAAAG GAAACATACT TACCTCTTTT CAACTCAACT CAAATTAAGA
      3913        3923        3933        3943        3953
ATAAGATACT CAACTCAAAG ATTAGGTATT CAACGCAAAT ATGGCACTCT
      3963        3973        3983        3993        4003
ACTCAATGAA GTACAAATTA ACTCAGGATA CTCGACTTAA GATACTCAAC
      4013        4023        4033        4043        4053
TCCCGACACT CAACTGAACT CATTTCAATA TAAAGCAGCT TAAAACAAGT
      4063        4073        4083        4093        4103
TCAGTATAAA GTAAAGTTGT TTAAAAACAT GATGTCAACT CTGTGTGTAT
      4113        4123        4133        4143        4153
AATAAGGGAT ACAACATAAC TTTGAAATGT ATATAAAAAT ACAATTAACT
```

FIGURE 7D

```
      4163        4173        4183        4193        4203
GATGTATATA AAAATACATT AATCTATGGG AGATTCTCTA ACCGACAACC
      4213        4223        4233        4243        4253
ATCACTTAAG GGCTAAGATG ATGATATAGC GATCTACCGC ACGCTGCCAT
      4263        4273        4283        4293        4303
CGCATCTTAT ACCCGGCCAA AGGTATAAGA CCTGAACTGC CTAATGAATC
      4313        4323        4333        4343        4353
CACTAATAAA CTGTTAAAAG GAATCATCTA AAAAGTATGA CCCTTTTCTA
      4363        4373        4383        4393        4403
CCCATAGTGG CTAACATGGT TTATGGGGGC TGTGAGTTAT CTGAACTCTC
      4413        4423        4433        4443        4453
CCCCATATCG GTGCTCAATA CTACTCCAAA AAATATACTG CTCTTATGTT
      4463        4473        4483        4493        4503
TAAAAACATA CTGATTCTGT GGTTTGAAAT TATTGCTTAA AGCTTAGATT
      4513        4523        4533        4543        4553
TTTGAAAAGC TCTCTTTTGA AAATCGTAGT TTCCTTTTTC TTCTATTAAA
      4563        4573        4583        4593        4603
GCTAGACATA GGCTATGTAG AACTCTAGCT TACCTTCCTT CTCAAAAGTT
      4613        4623        4633        4643        4653
TGAAAACATT TGCTTAGATT CTTAGGGACT ACTTAGTTCC CTTGTTGGAA
TTC
```

FIGURE 7E

PG GENOMIC

```
        10         20         30         40         50
AAGCTTCTTA AAAAGGCAAA TTGATTAATT TGAAGTCAAA ATAATTAATT

        60         70         80         90        100
ATAACAGTGG TAAAGCACCT TAAGAAACCA TAGTTTGAAA GGTTACCAAT

       110        120        130        140        150
GCGCTATATA TTAATCAACT TGATAATATA AAAAAAATTT CAATTCGAAA

       160        170        180        190        200
AGGGCCTAAA ATATTCTCAA AGTATTCGAA ATGGTACAAA ACTACCATCC

       210        220        230        240        250
GTCCACCTAT TGACTCCAAA ATAAAATTAT TATCCACCTT TGAGTTTAAA

       260        270        280        290        300
ATTGACTACT TATATAACAA TTCTAAATTT AAACTATTTT AATACTTTTA

       310        320        330        340        350
AAAATACATG GCGTTCAAAT ATTTAATATA ATTTAATTTA TGAATATCAT

       360        370        380        390        400
TTATAAACCA ACCAACTACC AACTCATTAA TCATTAAATC CCACCCAAAT

       410        420        430        440        450
TCTACTATCA AAATTGTCCT AAACACTACT AAAACAAGAC GAAATTGTTC

       460        470        480        490        500
GAGTCCGAAT CGAAGCACCA ATCTAATTTA GGTTGAGCCG CATATTTAGG

       510        520        530        540        550
AGGACACTTT CAATAGTATT TTTTTCAAGC ATGAATTTGA AATTTAAGAT

       560        570        580        590        600
TAATGGTAAA GAAGTAGTAC ATCCCGAATT AATTCATGCC TTTTTTAAAT

       610        620        630        640        650
ATAATTATAT AAATATTTAT GATTTGTTTT AAATATTAAA ACTTGAATAT

       660        670        680        690        700
ATTATTTTTT TAAAAATTAT CTATTAAGTA CCATCACATA ATTGAGACGA

       710        720        730        740        750
AGGAATAATT AAGATGAACA TAGTGTTTAA TTAGTAATGG ATGGGTAGTA
```

FIGURE 8A

```
      760         770         780         790         800
AATTTATTTA TAAATTATAT CAATAAGTTA AATTATAACA AATATTTGAG

      810         820         830         840         850
CGCCATGTAT TTTAAAAAAT ATTAAATAGT TTGAATTTAA AACCGTTAGA

      860         870         880         890         900
TAAATGGTCA ATTTTGAACC CAAAAGTGGA TGAGAAGGGT ATTTTAGAGC

      910         920         930         940         950
CAATAGGRGG ATGAGAAGGA TATTTTGAAG CCAATATGTG ATGGATGAAG

      960         970         980         990        1000
GATAATTTTG TATCATTTCT AATACTTTAA AGATATTTTA GGTCATTTTC

     1010        1020        1030        1040        1050
CCTTCTTTAG TTTATAGACT ATAGTGTTAG TTCATCGAAT ATCATCTATT

     1060        1070        1080        1090        1100
ATTTCCGTCT TAAATTATTT TTTATTTTAT AAATTTTTTA AAAATAAATT

     1110        1120        1130        1140        1150
ATTTTTTCCA TTTAACTTTG ATTGTAATTA ATTTTTAAAA ATTACCAACA

     1160        1170        1180        1190        1200
TATAAATAAA ATTAATATTT AACAAAGAAT TGTAACATAA TATTTTTTTA

     1210        1220        1230        1240        1250
ATTATTCAAA ATAAATATTT TTAAACATCA TATAAAAGAA ATACGACAAA

     1260        1270        1280        1290        1300
AAAATTGAGA CGGGAGAAGA CAAGCCAGAC AAAAATGTCC AAGAAACTCT

     1310        1320        1330        1340        1350
TTCGTCTAAA TATCTCTCAT CCAAACTAAT ATAATACCCA TTATAATTAA

     1360        1370        1380        1390        1400
CCATATTGAC CAACTCAAAC CCCTTAAAAT CTATAAATAG ACAAACCCTT

     1410        1420        1430        1440        1450
CCCATACCTC TTATCATAAA AAAAATAATA ATCTTTTTCA ATAGACAAGT

     1460        1470        1480        1490        1500
TTAAAAACCA TACCATATAA CAATATATCA TGGTTATCCA AAGGAATAGT
```

FIGURE 8B

```
      1510        1520        1530        1540        1550
ATTCTCCTTC TCATTATTAT TTTTGCTTCA TCAATTTCAA CTTGTAGAAG

      1560        1570        1580        1590        1600
CAATGTTATT GATGACAATT TATTCAAACA AGTTTATGAT AATATTCTTG

      1610        1620        1630        1640        1650
AACAAGAATT TGCTCATGAT TTTCAAGCTT ATCTTTCTTA TTTGAGCAAA

      1660        1670        1680        1690        1700
AATATTGAAA GCAACAATAA TATTGACAAG GTTGATAAAA ATGGGATTAA

      1710        1720        1730        1740        1750
AGTGATTAAT GTACTTAGCT TTGGAGCTAA GGGTGATGGA AAAACATATG

      1760        1770        1780        1790        1800
ATAATATTGT AAGTATTTAA ATATTGGAAT ATATTTGTGG GGATGAAAAT

      1810        1820        1830        1840        1850
GATAGAGAAT ATAAGAATTA TTTGGAAGGA TGAAAAGTTA TATTTTATAA

      1860        1870        1880        1890        1900
AGTAGAAAAT TATTTTCTCG TTTTTAGTAA TTAAAGGTGA AAAATGAGTT

      1910        1920        1930        1940        1950
TTCTCGTAAG CGAGGAAAGT CATTTTCCAT GGAACTGTAT TTTTTTTTTA

      1960        1970        1980        1990        2000
CTTTTAATAA CGTCATAGTA TTTGCTATAC TCAAGAATAA GACACTATTA

      2010        2020        2030        2040        2050
TTGATGTTTA GTGCTCGAAA AGAAATTGAT AGTAATTTTG CTAATATAAC

      2060        2070        2080        2090        2100
TATCAATTTC TTATATGTAT ATTTTTCAAC CAAAATAACA AAGCGTAATC

      2110        2120        2130        2140        2150
CAATAAGTGG GCCTCTAGAA TAAAGAGTAA GTTCTATTAA TTCTTAACCT

      2160        2170        2180        2190        2200
TATTTAATTT TATGGAAACC TCGACAAAAC GACAATGCTC AACTTATATT


CGAATTC
```

FIGURE 8C

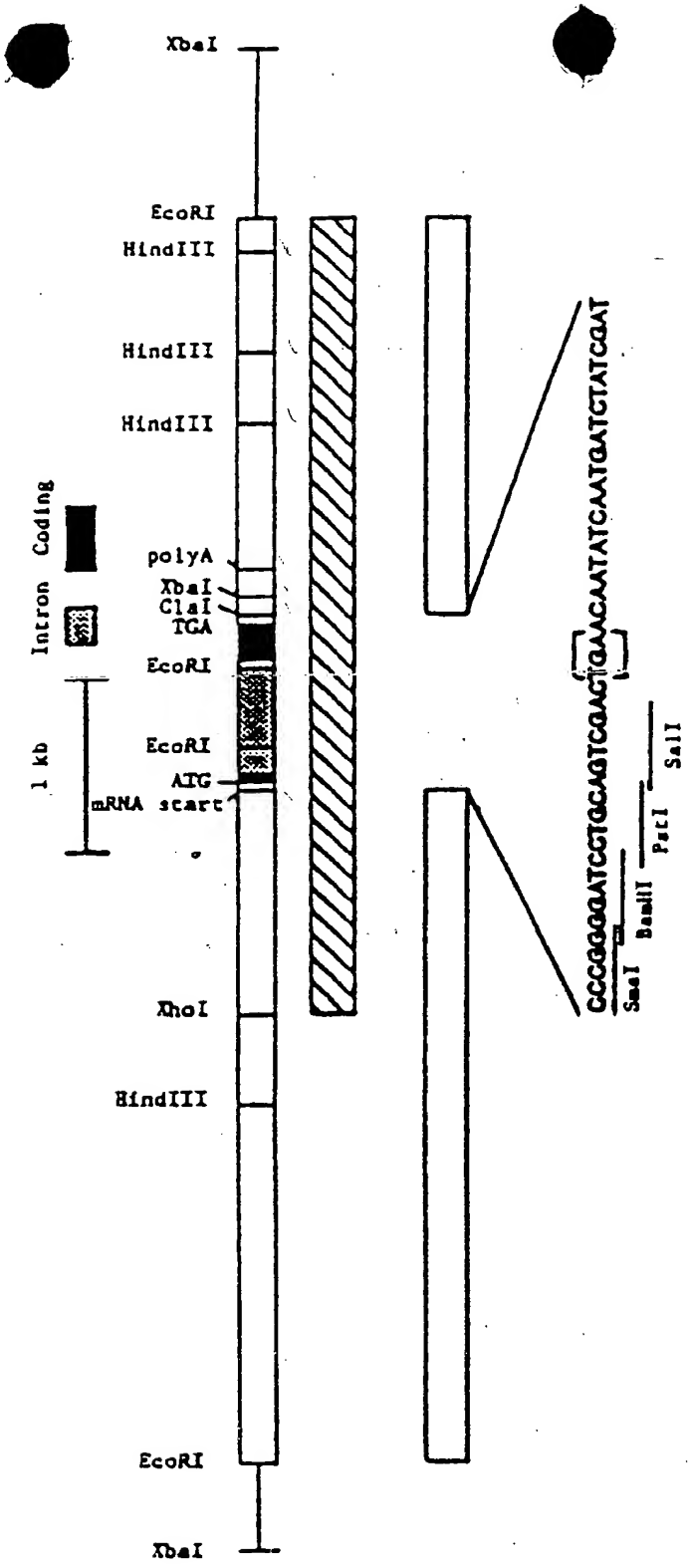
XbaI
EcoRI
HindIII
HindIII
HindIII
Intron Coding
polyA
XbaI
ClaI
TGA
EcoRI
1 kb
EcoRI
ATG
mRNA start
XhoI
HindIII
EcoRI
XbaI
SacI
BamII
PstI
SalI

FIGURE 9

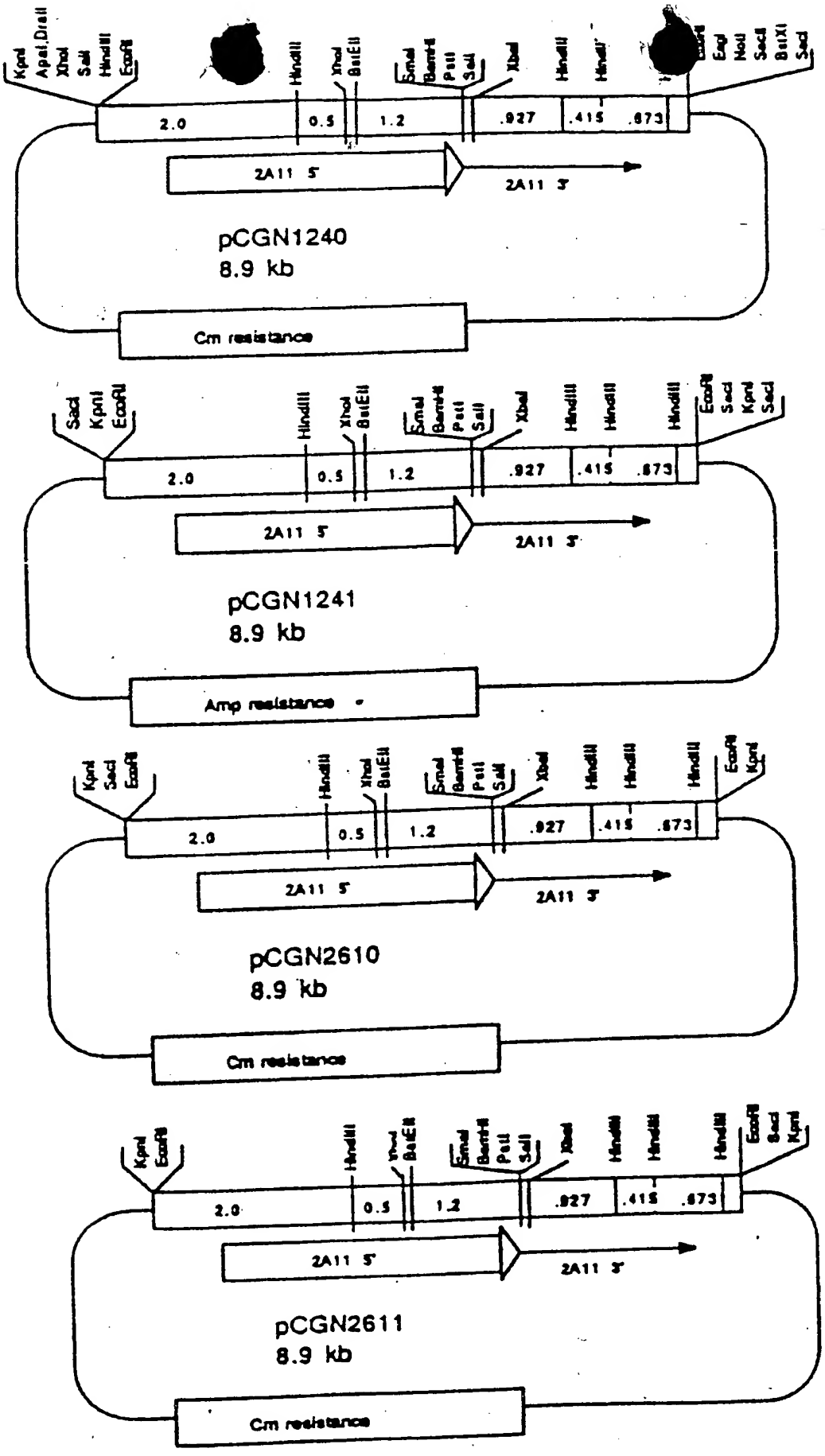
KpnI ApaI,DraII XhoI SalI HindIII EcoRI
HindIII XhoI BstEII SmaI BamHI PstI SalI XbaI HindIII HindIII
EcoRI EagI NotI SacII BstXI SacI
2.0 0.5 1.2 .927 .415 .673
2A11 5'
2A11 3'
pCGN1240
8.9 kb
Cm resistance
SacI KpnI EcoRI
HindIII XhoI BstEII SmaI BamHI PstI SalI XbaI HindIII HindIII HindIII
EcoRI SacI KpnI SacI
2.0 0.5 1.2 .927 .415 .673
2A11 5'
2A11 3'
pCGN1241
8.9 kb
Amp resistance
KpnI SacI EcoRI
HindIII XhoI BstEII SmaI BamHI PstI SalI XbaI HindIII HindIII HindIII
EcoRI KpnI
2.0 0.5 1.2 .927 .415 .673
2A11 5'
2A11 3'
pCGN2610
8.9 kb
Cm resistance
KpnI EcoRI
HindIII XhoI BstEII SmaI BamHI PstI SalI XbaI HindIII HindIII HindIII
EcoRI SacI KpnI
2.0 0.5 1.2 .927 .415 .673
2A11 5'
2A11 3'
pCGN2611
8.9 kb
Cm resistance

FIGURE 10